



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181983

TO: Robert M Kelly
Location: rem/2C55/2C70
Art Unit: 1633
Friday, March 17, 2006
Case Serial Number: 10/811028

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Kelly,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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STIC-Biotech/ChemLib

181983

mg

From: Kelly, Robert
Sent: Saturday, March 11, 2006 9:22 AM
To: STIC-Biotech/ChemLib
Subject: 10/811,028

RECEIVED
MAR 13 2006
(S16)

Please search:

SEQ ID NO: 1

Robert M. Kelly, Ph.D.
Art Unit 1633
Room 2C55, Remsen Bldg.
Mailbox 2C70
(571) 272-0729

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 19:41:09 ; Search time 20840 Seconds
(without alignments)
11816.019 Million cell updates/sec

Title: US-10-811-028A-1
Perfect score: 4331
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1923.8	44.4	3589	6	BD136051 Interfero
4	1845.4	42.6	8349	6	AR260588 Sequence
5	1836.8	42.4	2661	11	MI7626 Synthetic p
6	1821.8	42.1	2999	11	L38498 Cloning vec
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ALIGNMENTS

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LOCUS AX249944 3609 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 2 from Patent WO0166149.
ACCESSION AX249944
VERSION AX249944.1 GI:15864431
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fewell,J.G., MacLaughlin,F., Smith,L.C., Nicol,F. and Rolland,A.
TITLE Nucleic acid formulations for gene delivery and methods of use
JOURNAL Patent: WO 0166149-A 2 13-SEP-2001;
Valentis, Inc. (US)
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ORIGIN
Query Match 44.7%; Score 1937; DB 6; Length 3609;
Best Local Similarity 72.1%; Pred. No. 0;
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Db 26 CGTTACATACCTTACCGTAAATGCGCGCTGCTGACCGCCCAACGACCCCGCCCAT 85


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3494  AAACGATCTCTCATCTCTCTCTTGTATCAGATCTTGATCCCTCGGCCATCAG 3545

RESULT 2
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DEFINITION
Sequence 1 from Patent WO0166149.
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VERSION
AX249943.1 GI:15864429
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
REFERENCE
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AUTHORS
Fewell,J.G., MacLaughlin,F., Smith,L.C., Nicol,F. and Rolland,A.
TITLE
Nucleic acid formulations for gene delivery and methods of use
JOURNAL
Patent: WO 0166149-A 1 13-SEP-2001;
Valentis, Inc. (US)
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Qy 3200 AGCGGTGTTTTTTTGTTCAGACGACAGATACGCGCAGAAAAGAGATCTCAAGAA 3259
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Qy 3260 GATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGG 3319
Db 2619 GATCCTTTGATCTTTTCTACGGGTCTGACGC----- 2650
Qy 3320 ATTTGTGATAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGT 3379
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Qy 3380 CCGGCACATTTCCCGAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAGATGCG 3439
Db 2651 ----- 2650

Qy 3440 TAAGGAGAAATACCGCATCAGGAATTTGTAAGCTTAAATATTCAGAGAACTCGTCAA 3499
Db 2651 -----TCAGAGAACTCGTCAA 2667
Qy 3500 GAAGGCGATAGAAAGGCGATGCGCTGCGAATTCGGGAGCGGCGATACCGTAAAGACAGAGGA 3559
Db 2668 GAAGGCGATAGAAAGGCGATGCGCTGCGAATTCGGGAGCGGCGATACCGTAAAGACAGAGGA 2727
Qy 3560 AGCGGTACGCGCATTTGCGCGCGAAGCTCTTTACGCAATATCACGGGTAGCCAAACGCTATGT 3619
Db 2728 AGCGGTACGCGCATTTGCGCGCGAAGCTCTTTACGCAATATCACGGGTAGCCAAACGCTATGT 2787
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Db 3088 TTCATCAGCCATGATGATGATCTTTCGCGAGGACCAAGGTGAGATGACAGAGATCCT 3147
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RESULT 3
BD136051

LOCUS
DEFINITION

BD136051 3589 bp DNA linear PAT 18-SEP-2002
Interferon alpha plasmid and delivery system and method of
preparing and using the same.

ACCESSION

BD136051
BD136051.1 GI:23230996

VERSION

JP 2002506647-A/18.

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

other sequences; artificial sequences.

REFERENCE	1 (bases 1 to 3589)	
AUTHORS	Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.	
TITLE	Interferon alpha plasmid and delivery system and method of preparing and using the same	
JOURNAL	Patent: Jp 2002506647-A 18 05-MAR-2002;	
COMMENT	VALENTIS INC	
	OS Artificial Sequence	
	PN JP 2002506647-A/18	
	PD 05-MAR-2002	
	PF 12-MAR-1999 JP 2000536861	
	PR 19-MAR-1998 US 60/078654	
	PI JEFF NORDSTROM, FEDERICA, ALAIN ROLLAND, ROBERT RALSTON	
	PC C12N15/09, A61K38/21, A61K48/00, A61P35/00, C07K14/54, C07K14/56,	
	PC C12N1/15, A61K38/21, A61K48/00, A61P35/00, C07K14/54, C07K14/56,	
	PC C12N1/19, C12N1/21, C12N5/10/A61K9/127, C12N15/00, A61K37/66, PC	
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FEATURES	Location/Qualifiers	
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ORIGIN		
	Query Match 44.4%; Score 1923.8; DB 6; Length 3589;	
	Best Local Similarity 72.2%; Pred. No. 0;	
	Matches 2897; Conservative 0; Mismatches 603; Indels 512; Gaps 10;	
QY	321 CGTTTACATAACTTACGGTAAATGGCCCGCTGGCTGACGCGCCCAACGACCCCGGCCCATTT 380	
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QY	381 GACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGAATTTCCATTGACGTCA 440	
DB	61 GACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGAATTTCCATTGACGTCA 120	
QY	441 ATGGGTGGAGTATTACGGTAAACCTGGCCACCTTGGCAGTACATCAAGTGATCATATGCC 500	
DB	121 ATGGGTGGAGTATTACGGTAAACCTGGCCACCTTGGCAGTACATCAAGTGATCATATGCC 180	
QY	501 AAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTTGCCCAGTA 560	
DB	181 AAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTTGCCCAGTA 240	
QY	561 CATGACCTTATGGGACTTTCCTACTTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC 620	
DB	241 CATGACCTTATGGGACTTTCCTACTTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC 300	
QY	621 CATGCTGATGCGTTTTCGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAATCACGGGG 680	
DB	301 CATGCTGATGCGTTTTCGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAATCACGGGG 360	
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DB	361 ATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCACCAAAATCAAACG 420	
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QY	801 ACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAAACCGTTCAGATCGCTTGGAGACG 860	
DB	481 ACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAAACCGTTCAGATCGCTTGGAGACG 540	
QY	861 CCATCCAGCTGTTTGTGACCTCCATAGAGACACCGGACCGCATCCAGCGCTGACTCTAGC 920	
DB	541 CCATCCAGCTGTTTGTGACCTCCATAGAGACACCGGACCGCATCCAGCGCTGACTCTAGC 980	
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Db 3389 TAGCCTCTCCACCACGCGCGGAGAAACCTGCGTGAATCCATCTTGTTCAAATCATGCG 3448
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RESULT 4
AR260588 8349 bp DNA linear PAT 20-DEC-2002
LOCUS AR260588
DEFINITION Sequence 16 from patent US 6489542.
ACCESSION AR260588
VERSION AR260588.1 GI:27311143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8349)
AUTHORS Corbin,D.R. and Romano,C.P.
TITLE Methods for transforming plants to express Cry2Ab
delta.-endotoxins targeted to the plastids
JOURNAL Patent: US 6489542-A 16 03-DEC-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 42.6%; Score 1845.4; DB 6; Length 8349;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;

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Db 7229 AGGCGATCGGCTGCGAAATCGGAGCGGCGATACCGTAAAGCAGCAGGAGCGGTGAGGCC 7288
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Qy 3752 CTTGAGCTGCGCAACAGTTCCGGTGGCGGAGCCCTTGATGCTCTTCGTCCAGATCAT 3811
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RESULT 5

SYN8KMRG/c
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 DEFINITION Synthetic plasmid pK18 (pBRNeo/pUC18) kanamycin resistance gene,
 complete cds.
 ACCESSION M17626
 VERSION M17626.1 GI:207845
 KEYWORDS complete genome; kanamycin resistance.
 SOURCE unidentified cloning vector
 ORGANISM unidentified cloning vector
 other sequences; artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 2661)
 AUTHORS Pridmore,R.D.
 TITLE New and versatile cloning vectors with kanamycin-resistance marker
 JOURNAL Gene 56 (2-3), 309-312 (1987)
 PUBMED 3315864
 COMMENT Original
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ORIGIN

Query Match 42.4%; Score 1836.8; DB 11; Length 2661;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 1975; Conservative 0; Mismatches 102; Indels 57; Gaps 2;
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Qy 4179 ATCAGAGCGCGATTTGCTGTGTGTCGCCAGTCATAGCCGATAGCTCTCCACCCAGC 4238
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Qy 4239 GCGCGGAGAACCTTCGTCGAATCCATCTTTGTTCAATCATGCGAAACGATCATCTGT 4298
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Db 343 CTCCTGATCAGATCTTTGATCCCTTCGCCCATCAG 310
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LOCUS SYNCCDBA 2999 bp DNA linear SYN 16-MAR-2000
DEFINITION Cloning vector pKil118 ccdB gene, complete cds and
kanamycin-resistance (Kmr) gene fragment.
ACCESSION L38498
VERSION L38498.1 GI:986977
KEYWORDS ccdB gene; cloning vector; kanamycin resistance.
SOURCE Cloning vector pKil118
ORGANISM Cloning vector pKil118
REFERENCE 1 (bases 1 to 2999)
AUTHORS Bernard, P.
TITLE New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers
JOURNAL Gene 162 (1), 159-160 (1995)
PUBMED 7557407
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ORIGIN
Query Match      42.1%; Score 1821.8; DB 11; Length 2999;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches 102; Indels 57; Gaps 2;
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DB |||||
QY 899 TGATCCCGCTGCGCATCAG 881
DB |||||

RESULT 7
SYNCCDBB/c 2999 bp DNA linear SYN 16-MAR-2000
LOCUS Cloning vector pKILL19 ccdB gene, complete cds and
DEFINITION kanamycin-resistance gene (KmR) gene fragment.
L38499
ACCESSION L38499.1 GI:986979
VERSION ccdB gene; kanamycin resistance.
KEYWORDS Cloning vector pKILL19
SOURCE Cloning vector pKILL19
ORGANISM other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2999)
AUTHORS Bernard,P.
TITLE New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers
JOURNAL Gene 162 (1), 159-160 (1995)
PUBMED 7557407
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Query Match 42.1%; Score 1821.8; DB 11; Length 2999;
Best Local Similarity 92.5%; Pred. No. 0;
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Db	2939	GCATAAAGTGTAAAGCTCGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGTTGC	2880
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Qy	4134	AAAAAGAAACCGGCGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4193
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Qy	4194	TGCTGTTGTCGCGAGTCTAGCCGATGCTTCCACCCAGCGCGCGGAGAACCTGC	4253
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Qy	4254	GTGCAATCCATCTGTTCAATCATGCAAAACGATCCTCATCTGCTCTTGTATCAGAGCT	4313
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RESULT 10
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 DEFINITION His-3 integration vector pJHAM002, complete sequence.
 ACCESSION AY189827
 VERSION AY189827.1 GI:28435537
 KEYWORDS his-3 integration vector pJHAM002
 SOURCE his-3 integration vector pJHAM002
 ORGANISM his-3 integration vector pJHAM002
 other sequences; artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 11373)
 Lee,D.W., Haag,J.R. and Aramayo,R.
 AUTHORS Construction of strains for rapid homokaryon purification after
 TITLE Integration of constructs at the histidine-3 (his-3) locus of
 Neurospora crassa
 JOURNAL Curr. Genet. 43 (1), 17-23 (2003)
 PUBMED 12684841
 REFERENCE 2 (bases 1 to 11373)
 Lee,D.W., Haag,J.R. and Aramayo,R.
 AUTHORS Direct Submission
 TITLE Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
 JOURNAL College Station, TX 77843-3258, USA

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 ACCESSION BD063789
 VERSION BD063789.1 GI:22609392
 KEYWORDS JP 2001505435-A/2.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 3600)
 AUTHORS Coleman, M., Schwartz, R. and Demayo, F. J.
 TITLE Insulin-like growth factor I (IGF)-1 expression system and methods of

JOURNAL Patent: JP 2001505435-A 2 24-APR-2001;
 COMMENT BARENTIS INC. BAYLOR COLLEGE OF MEDICINE
 PN JP 2001505435-A/2
 PD 24-APR-2001
 PF 01-DEC-1997 JP 1998525696
 PR 02-DEC-1996 US 60/031539, 19-NOV-1997 US 08/974572 PI
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ACCESSION	BD069040				
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REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 3600)				
TITLE	Coleman,M.				
JOURNAL	Treatment for urinary incontinence using gene therapy techniques				
COMMENT	Patent: JP 2001511154-A 2 07-AUG-2001;				
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DEFINITION	BD136049	Interferon alpha plasmid and delivery system and method of preparing and using the same.	
ACCESSION	BD136049		
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SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
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AUTHORS		Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.	
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 Db 1453 GCTCACGCTGAGGTATCTCAGTTCGGTGTAGTTCGCTTCCAAAGCTGGGCTGTGTC 1512
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RESULT 15
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 AUTHORS
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 Brown, P.A., Draghia-Akli, R. and Carpenter, R.H.
 Reducing culling in herd animals growth hormone releasing
 hormone (ghrh)

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Query Match	39.7%; Score 1718.4; DB 6; Length 3534;
Best Local Similarity	90.5%; Pred. No. 0;
Matches 1926; Conservative	0; Mismatches 11; Indels 191; Gaps 1;
QY	2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTTCAGGGTTAAATTCGAGCTTGGCGTAATCAT 2264
DB	1366 GGCCCGGTACCAGCTTTTGTTCCTTTAGTTCAGGGTTAAATTCGAGCTTGGCGTAATCAT 1425
QY	2265 GGTATAGCTGTTCCTGTGTGAATTCCTATCCGCTCACAAATCCACACAAATACGAG 2324
DB	1426 GGTATAGCTGTTCCTGTGTGAATTCCTATCCGCTCACAAATCCACACAAATACGAG 1485
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QY	2445 TCGGCCAACGCGCGGGAGAGCGGTTTGCCTATTTGGCGCTCTTCCGCTTCCCTCGCTCA 2504
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QY	2505 CTGACTCGCTCGCTCGCTGCTGCTGCGGAGCGGTATGAGTCACTCAAAAGCGG 2564
DB	1666 CTGACTCGCTCGCTCGCTGCTGCTGCGGAGCGGTATGAGTCACTCAAAAGCGG 1725
QY	2565 TAATACGGTTATCCACAGATCAGGGGATACGAGGAGAAAGATGAGCAAAAGGCC 2624
DB	1726 TAATACGGTTATCCACAGATCAGGGGATACGAGGAGAAAGATGAGCAAAAGGCC 1785
QY	2625 AGCAAAAGCCAGGAAACCGTAAAGAGCGGTTGCTGCGGTTTTTCATAGGCTCCGCC 2684
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QY	3585	CTCTTTACGAATATCACGGGTAGCCAAACGCTATGTCTGTAGTAGCGGTTCGCGCTGGC	3644
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QY	3645	CCGGCCACAGTCGATGAATCCAGAAAAAGCGGCCATTTTCCACCATGATATTTGGGCAAGCA	3704
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QY	3705	GGCATCGCATGGGTTCACGAGAGATCTCCGCGTGGGCGATGCTCGCTTTGAGCTGGC	3764
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QY	3765	GAAAGTTTCGCTGGCGGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAAG	3824
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Db	2795	ACCGGTTTCCATCCGAGTACGTGCTCGCTCGATGGGATGTTTCGCTTGGTGGTCCAAATGG	2854
QY	3885	GCAGTACCGGATCAAGCGGTATGAGCGCGCATTCGATCGCATGATGGATCTTTT	3944
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QY	4125	GCTCTTGACAAAGAAACCGGCGCCCTGCGCTGACAGCGGAAACACGCGGCGCATCAGA	4184
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Qy	4185	GCAGCGATTGCTGTGTGTCGCCAGTCATAGCCGAATAGCCTCTCCACCCAAAGCGCGG	4244
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Search completed: March 16, 2006, 01:29:29
Job time : 20887 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 19:30:36 ; Search time 2263 Seconds
(without alignments)

12758.042 Million cell updates/sec

Title: US-10-811-028A-1

Perfect score: 4331

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3245.6	74.9	4187	13	ADT55140
4	3147.8	72.7	4058	13	ADT55139
5	2341.8	54.1	5753	13	ADT55137
6	2341.8	54.1	5760	13	ADT55138
7	1937	44.7	3609	5	AAI70085
8	1924.4	44.4	3589	5	AAI70084
9	1923.8	44.4	3589	2	AAZ40418
10	1923.8	44.4	3589	12	ADP77242
11	1845.4	42.6	8349	3	AAAI5565
12	1844.4	42.6	11546	13	ADU73266
13	1719	39.7	3600	2	AAV50427
14	1719	39.7	3600	2	AAV40795
15	1719	39.7	5707	2	AAH80055
16	1718.4	39.7	2192	6	ABQ78294
17	1718.4	39.7	3026	10	AAZ53819
18	1718.4	39.7	3426	2	AAZ40416
19	1718.4	39.7	3426	12	ADF77240

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27	1718.4	39.7	3534	9	AAAL60444
28	1718.4	39.7	3534	9	AAAL60445
29	1718.4	39.7	3534	9	AAAL60446
30	1718.4	39.7	3534	9	AAAL60447
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ALIGNMENTS

RESULT 1

ADT55135

ID ADT55135 standard; DNA; 4332 BP.

XX

AC ADT55135;

XX

DT 30-DEC-2004 (first entry)

XX

DE Nucleotide sequene of expression vector pMB1-MnSOD.

XX

KW Ophthalmological; radiation; free radical; superoxide anion;
 heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
 glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;
 xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
 graft-versus-host disease; systemic lupus erythematosus;
 rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
 psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.

OS Homo sapiens.

OS Simian virus 40.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 2..781

FT FT /*tag= a

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FT intron 332..497

FT FT /*tag= b

FT polyA_signal /note= "human beta-globin intron"

FT FT /*tag= c

FT FT /note= "SV40 late gene polyadenylation signal"

FT promoter 471..1162

FT FT /*tag= d

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FT FT /note= "ColE1 ori from pBluescript SK+"

FT CDS 1236..2020

FT FT /*tag= f

FT /gene= "kanamycin resistance gene"

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Db		1921	CGTTATCTCGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA	1980
Qy		1981	AAAAAACGGAATTCCTCGACCCGGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG	2040
Db		1981	AAAAAACGGAATTCCTCGACCCGGGGGATCCACTAGTTCTAGAGCGCGCGCCACCGCG	2040
Qy		2041	GTGGAGCTCCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAAATTTGTGATGC	2100
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Db		2101	TATTGCTTTATTGTGTAAACCATTAATAAGCTGCAATAAAACAAAGTTTAAACAAATTTGCATTCA	2160
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Qy		2221	TTGTTTCCCTTTAGTGAGGGTTTAATTTTCGAGCTTGGCGTATCATGGTTCATAGCTGTTTCC	2280
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Qy		2281	TGTTGTGAATTTGTTTATCCGCTTCACAATTCACACAACATACGAGCCGGGAAGCATAAAGTG	2340
Db		2281	TGTTGTGAATTTGTTTATCCGCTCACAATTCACACAACATACGAGCCGGGAAGCATAAAGTG	2340
Qy		2341	TAAAGCCTTGGGGTGCCTTAATAGTAGAGCTAACTCACATTAATTGCGTTGGCTCACTGCC	2400
Db		2341	TAAAGCCTTGGGGTGCCTTAATAGTAGAGCTAACTCACATTAATTGCGTTGGCTCACTGCC	2400
Qy		2401	CGCTTTCCAGTCGGGNAACCTGTCGTCGACGTGCATTATGAATCGGCCAAACGCGCGGG	2460
Db		2401	CGCTTTCCAGTCGGGNAACCTGTCGTCGACGTGCATTATGAATCGGCCAAACGCGCGGG	2460
Qy		2461	GAGAGGCGGTTTGGGTATTGGGCGCTCTTTCGCTTCTCGCTCACTGACTCGCTCGCGCTC	2520
Db		2461	GAGAGGCGGTTTGGGTATTGGGCGCTCTTTCGCTTCTCGCTCACTGACTCGCTCGCGCTC	2520
Qy		2521	GGTCGTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGGTAATACGGTTATCCAC	2580
Db		2521	GGTCGTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGGTAATACGGTTATCCAC	2580

QY	2581	AGAAATCAGGGGATAAACGACGAAAGAAACATGTGAGCNAAGAGCCAGCAAAAGGCCACAGGAA	2640
DB	2581	AGAAATCAGGGGATAAACGACGAAAGAAACATGTGAGCNAAGAGCCAGCAAAAGGCCACAGGAA	2640
QY	2641	CCGTAAAAAGGCGCGGTGTGCTGCGTTTTTCCATAGGCTCCGCGCCCTGACGAGCATCA	2700
DB	2641	CCGTAAAAAGGCGCGGTGTGCTGCGTTTTTCCATAGGCTCCGCGCCCTGACGAGCATCA	2700
QY	2701	CAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATATAAGATACACAGGC	2760
DB	2701	CAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATATAAGATACACAGGC	2760
QY	2761	GTTCCTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTTCGACACCTCGCGCTTACCCGATA	2820
DB	2761	GTTCCTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTTCGACACCTCGCGCTTACCCGATA	2820
QY	2821	CCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTA	2880
DB	2821	CCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTA	2880
QY	2881	TCTCAGTTCCGCTGATAGTTCGCTCCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCA	2940
DB	2881	TCTCAGTTCCGCTGATAGTTCGCTCCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCA	2940
QY	2941	GCCCGACCGCTGGCGCTTATCCGCTAACTATCGCTTTAGTCCAAACCCGCTAAGACACGA	3000
DB	2941	GCCCGACCGCTGGCGCTTATCCGCTAACTATCGCTTTAGTCCAAACCCGCTAAGACACGA	3000
QY	3001	CTTATCCGCACTGGCAGCAGCCACTGGTAAACAGATTTAGCAGACGAGGTATGTAGCGG	3060
DB	3001	CTTATCCGCACTGGCAGCAGCCACTGGTAAACAGATTTAGCAGACGAGGTATGTAGCGG	3060
QY	3061	TGCTACAGAGTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAAGACAGTATTGG	3120
DB	3061	TGCTACAGAGTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAAGACAGTATTGG	3120
QY	3121	TATCTGCGCTCTGCTGAAGCAGTTACTTTTCGGAAAAAGAGTTGGTAGTCTCTTGATCCGG	3180
DB	3121	TATCTGCGCTCTGCTGAAGCAGTTACTTTTCGGAAAAAGAGTTGGTAGTCTCTTGATCCGG	3180
QY	3181	CAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAACAAAGAGTTCTGATCCGG	3240
DB	3181	CAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAACAAAGAGTTCTGATCCGG	3240
QY	3241	AAAAAAAGGATCTCAAGAAGATCCTTTTGATCTTTCTACGGGGTCTGACGCTCAAGTGAA	3300
DB	3241	AAAAAAAGGATCTCAAGAAGATCCTTTTGATCTTTCTACGGGGTCTGACGCTCAAGTGAA	3300
QY	3301	CGAAAACTCAGTTAAGGGATTTTGTTCATGAGGGATACATATTTGAAATGTTATTAGAA	3360
DB	3301	CGAAAACTCAGTTAAGGGATTTTGTTCATGAGGGATACATATTTGAAATGTTATTAGAA	3360
QY	3361	AAATAAAACAAATAGGGGTTCCGGCGCAATTTCCCGAAAAAGTCCACTGTATGCGGTGT	3420
DB	3361	AAATAAAACAAATAGGGGTTCCGGCGCAATTTCCCGAAAAAGTCCACTGTATGCGGTGT	3420
QY	3421	GAATAACCGCACAGATCGTTAAGAGAAATAACCGCATAGGAAATTTGTAAGCGTTAATA	3480
DB	3421	GAATAACCGCACAGATCGTTAAGAGAAATAACCGCATAGGAAATTTGTAAGCGTTAATA	3480
QY	3481	ATTTCAGAAAGAACTCGTCAAGAAAGCGATAGAAGCGATGCGCTCGCAATCGGAGCGCGG	3540
DB	3481	ATTTCAGAAAGAACTCGTCAAGAAAGCGATAGAAGCGATGCGCTCGCAATCGGAGCGCGG	3540
QY	3541	ATACCGTAAAGACAGAGAAAGCGGTACGCCATTTCCGCGCCAAAGCTCTTCAGCAATATCA	3600
DB	3541	ATACCGTAAAGACAGAGAAAGCGGTACGCCATTTCCGCGCCAAAGCTCTTCAGCAATATCA	3600
QY	3601	CGGCTACCAACGCTATGCTCTGATAGCGGTTCGCCACACCCAGCGGGCCACAGTCGATG	3660
DB	3601	CGGCTACCAACGCTATGCTCTGATAGCGGTTCGCCACACCCAGCGGGCCACAGTCGATG	3660
QY	3661	AATCCAGAAAGCGGCCATTTTCCACCATGATATTTCGGCAAGCAGGCGATCCCATGGGTC	3720

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3661 AATCAGAAAAGCGCCATTTTCCACCATGATATTCCGCAAGCAGGCATGCCATGGTGC 3720
|||||
3721 ACGACGAGATCCTCGCGTCGGGATGCTCGCCCTTGAGCCTGGGCAACAGATTCCGCTGGC 3780
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3721 ACGACGAGATCCTCGCGTCGGGATGCTCGCCCTTGAGCCTGGGCAACAGATTCCGCTGGC 3780
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3781 CGGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAGACCGGCTTCCATCCGA 3840
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3781 CGGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAGACCGGCTTCCATCCGA 3840
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3841 GTACGTGCTCGTCGATCGATGTTTCGCTTGGTGGTGAATGGCAGGTAGCCGGATCA 3900
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3841 GTACGTGCTCGTCGATCGATGTTTCGCTTGGTGGTGAATGGCAGGTAGCCGGATCA 3900
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3901 AGCGTATCGAGCCCGCATTCGATCGACGATGATGATCTTTCTCGGAGGAGCAAGG 3960
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3901 AGCGTATCGAGCCCGCATTCGATCGACGATGATGATCTTTCTCGGAGGAGCAAGG 3960
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3961 TGAGATGACAGAGATCTCTGCCCGGCACTTTCGCCCAATAGCAGCCAGTCCCTTCCCGCT 4020
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3961 TGAGATGACAGAGATCTCTGCCCGGCACTTTCGCCCAATAGCAGCCAGTCCCTTCCCGCT 4020
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4021 TCAGTGACAGCTCGACGACAGCTCGCAAGGAAGCCGCTCGTGGCCAGCCAGATAGC 4080
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4021 TCAGTGACAGCTCGACGACAGCTCGCAAGGAAGCCGCTCGTGGCCAGCCAGATAGC 4080
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4081 CGCGTGTGCTGCTCTTTCGAGTTCACTTCAGGGCACCGGACAGTCTTGACAAAAGA 4140
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4081 CGCGTGTGCTGCTCTTTCGAGTTCACTTCAGGGCACCGGACAGTCTTGACAAAAGA 4140
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4141 ACCGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGATCAGACGACCGATTTCTGT 4200
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4141 ACCGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGATCAGACGACCGATTTCTGT 4200
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4201 TGTCGCCAGTACAGCGAATAGCTCTCCACCGAGCGCGGAGAACCTCGTGCAT 4260
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4201 TGTCGCCAGTACAGCGAATAGCTCTCCACCGAGCGCGGAGAACCTCGTGCAT 4260
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4261 CCATCTTGTTCATCATCGAAACGATCTCATCTCTGCTCTTGATCAGAGCTTGATCCC 4320
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4261 CCATCTTGTTCATCATCGAAACGATCTCATCTCTGCTCTTGATCAGAGCTTGATCCC 4320
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4321 CTGCGCCATCAG 4332
|||||
4321 CTGCGCCATCAG 4332

RESULT 2
ADT55136
ID ADT55136 standard; DNA; 4293 BP.

AC ADT55136;

XX 30-DEC-2004 (first entry)

DE Nucleotide sequence of expression vector pMB1-HA-MnSOD.

XX Ophthalmological; radiation; free radical; superoxide anion;
KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;
KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.

XX Homo sapiens.

OS Simian virus 40.

OS Synthetic.

XX Key Location/Qualifiers

FT 2..781

FT CDS /*tag= a

FT intron /note= "human Manganese superoxide dismutase cDNA"
FT 332..497
FT /*tag= b
FT /note= "human beta-globin intron"
FT 347..503
FT /*tag= c
FT /note= "SV40 late gene polyadenylation signal"
FT 471..1162
FT /*tag= d
FT /note= "CMV promoter"
FT 1158..1825
FT /*tag= e
FT /note= "ColE1 ori from pBluescript SK+"
FT 1226..2020
FT /*tag= f
FT /gene= "kanamycin resistance gene"

PN WO2004087873-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009194.

XX 26-MAR-2003; 2003US-0458793P.

PR 25-MAR-2004; 2004US-07778889.

XX (GENT-) GENTERIC INC.

XX Bennett MJ, Chen Y;

PI WPI; 2004-737685/72.

DR Claim 34; SEQ ID NO 2; 58pp; English.

XX The specification describes a method for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell. The method comprises contacting the cell with one or more nucleic acids encoding proteins that neutralizes or eliminates a portion of free radicals.

XX The specification describes a method for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell. The method comprises contacting the cell with one or more nucleic acids encoding one or more proteins that are expressed in the cell and that neutralizes or eliminates a portion of the free radicals, superoxide anions or heavy metal cations in the cell. The proteins are selected from metallothionein, superoxide dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl transpeptidase. The method is useful for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell, and ameliorating symptoms of xerostomia or xerophthalmia associated with conditions such as autoimmune disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic dysfunction, conditions affecting the CNS, psychogenic disorder, trauma, hepatitis C, cancer and decrease in mastication. The present sequence represents an expression vector used in the method of the invention to express the relevant proteins.

XX Query Match 96.3%; Score 4170.6; DB 13; Length 4293;

XX Best Local Similarity 98.2%; Pred. No. 0;

XX Matches 454; Conservative 0; Mismatches 39; Indels 39; Gaps 2;

QY 1 CGGTGCGGCGCTCTTCGCTATTACGCCAGCTGCGGAAGGGGGATGCTGTCGAAGCGAT 60
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Dd 1 CGGTGCGGCGCTCTTCGCTATTACGCCAGCTGCGGAAGGGGGATGCTGTCGAAGCGAT 60
|||||
QY 61 TAAGTTGGTGAACGCCAGGGTTTTCCAGTCACAGCTTGTAAACACGCGGCAGTGAAT 120
|||||
Dd 61 TAAGTTGGTGAACGCCAGGGTTTTCCAGTCACAGCTTGTAAACACGCGGCAGTGAAT 120
|||||
QY 121 TGTAAATACGACTCACTATAGGGCGGAATTGGGTACTTGGCCACAGAGCTTGGCCCATTTGCAT 180

Db 121 TGTATACGACTCACTAGGCGGAATTGGGTACTGGCCACAGAGCTTGGCCCATTCAT 180
QY 181 AGTTGTATCCATATCAATATATGACATTTATATTTGGTCTATGTCGAACATTAACCGCA 240
Db 181 AGTTGTATCCATATCAATATATGACATTTATATTTGGTCTATGTCGAACATTAACCGCA 240
QY 241 TGTGACATTTGATTTAGTACAGTTATTAATAGTAAATCAATTAAGGGGTCAATAGTTTCAT 300
Db 241 TGTGACATTTGATTTAGTACAGTTATTAATAGTAAATCAATTAAGGGGTCAATAGTTTCAT 300
QY 301 AGCCATATATGGAGTTCCGGTTTACATTAACCTTACGGTAAATGGCCCGCTTGGCTGACCG 360
Db 301 AGCCATATATGGAGTTCCGGTTTACATTAACCTTACGGTAAATGGCCCGCTTGGCTGACCG 360
QY 361 CCCAAGCAGCCCGCCCAATGACGTCAATATAGTATGATGTTCCCATAGTAACGCCAATA 420
Db 361 CCCAAGCAGCCCGCCCAATGACGTCAATATAGTATGATGTTCCCATAGTAACGCCAATA 420
QY 421 GGGACTTTTCCATTTGACGTCAATGGGTGGAGTATTTACGGTAAACTGGCCCACTTGGCAGTA 480
Db 421 GGGACTTTTCCATTTGACGTCAATGGGTGGAGTATTTACGGTAAACTGGCCCACTTGGCAGTA 480
QY 481 CATCAAGTGTATCATATGCCAAGTACGCCCCCTTATGACGTCAATGACGTAAATGGCCC 540
Db 481 CATCAAGTGTATCATATGCCAAGTACGCCCCCTTATGACGTCAATGACGTAAATGGCCC 540
QY 541 GCCTGGCATATGCCAGTACATGACCTTATGGGACTTTTCCCTTGGCAGTACATCTAC 600
Db 541 GCCTGGCATATGCCAGTACATGACCTTATGGGACTTTTCCCTTGGCAGTACATCTAC 600
QY 601 GTATTAGTCATCGCTATTACCATGGTGTATGGGTTTTGGCAGTACATCAATGGCGGTGA 660
Db 601 GTATTAGTCATCGCTATTACCATGGTGTATGGGTTTTGGCAGTACATCAATGGCGGTGA 660
QY 661 TAGCGTTTGTACTACGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTG 720
Db 661 TAGCGTTTGTACTACGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTG 720
QY 721 TTTTGGCACAAAATCAACGGGACTTTCCAAAATGTGTAACTCCGCCCATTTGACG 780
Db 721 TTTTGGCACAAAATCAACGGGACTTTCCAAAATGTGTAACTCCGCCCATTTGACG 780
QY 781 CAAATGGCGGTAGCGGTGACGGTGGAGGTCTATATAAGCAGAGCTCGTTTGTAGTAAC 840
Db 781 CAAATGGCGGTAGCGGTGACGGTGGAGGTCTATATAAGCAGAGCTCGTTTGTAGTAAC 840
QY 841 CGTCAGATCGCTCGAGACGCCATCCAGCTGTTTGGACCTCCATAGAACACCGGGAC 900
Db 841 CGTCAGATCGCTCGAGACGCCATCCAGCTGTTTGGACCTCCATAGAACACCGGGAC 900
QY 901 CGATCCAGCCTGACTTAGCTAGCTCTGAAAGTTGGTGGAGCCCTGGGAGGTTGGT 960
Db 901 CGATCCAGCCTGACTTAGCTAGCTCTGAAAGTTGGTGGAGCCCTGGGAGGTTGGT 960
QY 961 ATCAAGGTTTACAAGACAGGTTTAAAGGAGACCAATAGAACTGGGCACTGTGGAGACAGAGA 1020
Db 961 ATCAAGGTTTACAAGACAGGTTTAAAGGAGACCAATAGAACTGGGCACTGTGGAGACAGAGA 1020
QY 1021 AGACTCTTGGTTTCTGATAGGCACTGACTCTCTCTGCGCTATTTGGTCTATTTTCCACCC 1080
Db 1021 AGACTCTTGGTTTCTGATAGGCACTGACTCTCTCTCTGCGCTATTTGGTCTATTTTCCACCC 1080
QY 1081 TTAGGCTGCTGCTGAGCTAGGAGATCTCTCGAGGTTCGACGGTATCGATAGCTTTGAT 1140
Db 1081 TTAGGCTGCTGCTGAGCTAGGAGATCTCTCGAGGTTCGACGGTATCGATAGCTTTGAT 1140
QY 1141 ATCGAAATTCGGGCGGCGAGGACGGCACTCGTGGCTGTGGTGGCTTCGGCAGCGGCTT 1200
Db 1141 AATTCACCATGGCTTC-----TAGCCCTTATGACGTGCTGACTATGCGAGTTTAGG 1193
QY 1201 CAGCAGATCGCGGCACTACGGGTAGCACACGACTAGCAGCATGTTGAGCCGGGAGTG 1260

Db 1194 AGGACCTTCT-----ATGTTGAGCGCGGCACTG 1221
QY 1261 TGGCGCACACGAGGAGCTGGCTCCGGTTTTTGGGGTATCTGGGCTCCAGGCAGAACAC 1320
Db 1222 TGGCGCACACGAGGAGCTGGCTCCGGTTTTTGGGGTATCTGGGCTCCAGGCAGAACAC 1281
QY 1321 AGCCTCCCGACCTTGGCTTACGACTAGCGGGCCCTGGAACCTCACATCAACCGCGCAGATC 1380
Db 1282 AGCCTCCCGACCTTGGCTTACGACTAGCGGGCCCTGGAACCTCACATCAACCGCGCAGATC 1341
QY 1381 ATGAGCTGACACACACAGCAACGCGGCTTACGTGAACAACTGGAACGCTCACCGAG 1440
Db 1342 ATGAGCTGACACACAGCAACGCGGCTTACGTGAACAACTGGAACGCTCACCGAG 1401
QY 1441 GAGAAGTACACAGGAGGCTTGGCCCAAGGGAGATGTTACAGCCAGATAGCTTTCAGCCT 1500
Db 1402 GAGAAGTACACAGGAGGCTTGGCCCAAGGGAGATGTTACAGCCAGATAGCTTTCAGCCT 1461
QY 1501 GCACTGAAGTTCAATGGTGGTGTATCAATCATAGCATTTTCTGGACAAACCTCAGC 1560
Db 1462 GCACTGAAGTTCAATGGTGGTGTATCAATCATAGCATTTTCTGGACAAACCTCAGC 1521
QY 1561 CCTAACCGTGTGAGAACCCAAAGGGAGTGTCTGGAAGCCATCAAACTGATCTTGGT 1620
Db 1522 CCTAACCGTGTGAGAACCCAAAGGGAGTGTCTGGAAGCCATCAAACTGATCTTGGT 1581
QY 1621 TCCTTTGACAAAGTTTAAAGGAGAGCTGACGCTGCTATCTGTTGGTGTCCAGGCTCAGGT 1680
Db 1582 TCCTTTGACAAAGTTTAAAGGAGAGCTGACGCTGCTATCTGTTGGTGTCCAGGCTCAGGT 1641
QY 1681 TGGGGTTGGCTTGGTTTTCAATAAGGAACGGGGACACTTACAAATGCTGCTTGTCCAAAT 1740
Db 1642 TGGGGTTGGCTTGGTTTTCAATAAGGAACGGGGACACTTACAAATGCTGCTTGTCCAAAT 1701
QY 1741 CAGGATCCACTGCAAGAACAAAGGCTTATTTCCACTGCTGGGGATGATGTGGAG 1800
Db 1702 CAGGATCCACTGCAAGAACAAAGGCTTATTTCCACTGCTGGGGATGATGTGGAG 1761
QY 1801 CAGCTTACTTACTTTCAGTATAAAATGTTCAGGCTGATTTATCTATAAAGCTTATTTGGAT 1860
Db 1762 CAGCTTACTTACTTTCAGTATAAAATGTTCAGGCTGATTTATCTATAAAGCTTATTTGGAT 1821
QY 1861 GTAATCAACTGGGGAGATTAATCTGAAAGATACATGCTTGTGAAAAAGTAAACCCAGAT 1920
Db 1822 GTAATCAACTGGGGAGATTAATCTGAAAGATACATGCTTGTGAAAAAGTAAACCCAGAT 1881
QY 1921 CGTTATGCTCGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA 1980
Db 1882 CGTTATGCTGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA 1941
QY 1981 AAAAAACGGAAATTCCTGACGCGCGGGGATCCACTAGTTCTAGAGCGCGCCGACCGCG 2040
Db 1942 AAAAAACGGAAATTCCTGACGCGCGGGGATCCACTAGTTCTAGAGCGCGCCGACCGCG 2001
QY 2041 GTGAGCTCCAACTAGAAATGCAAGTGAAGAAAAATGCTTTATTTGTGAAAAATTTGTGATGC 2100
Db 2002 GTGAGCTCCCAACTAGAAATGCAAGTGAAGAAAAATGCTTTATTTGTGAAAAATTTGTGATGC 2061
QY 2101 TATTGCTTTTATTTGTAACCAATTAAGCTCAATTAACCAATTAACCAATTAACCAATTA 2160
Db 2062 TATTGCTTTTATTTGTAACCAATTAAGCTCAATTAACCAATTAACCAATTAACCAATTA 2121
QY 2161 TTTTATGTTTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2220
Db 2122 TTTTATGTTTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2181
QY 2221 TTGTTCCCTTTTATGAGGTTTAAATTTTCAGCTTGGGCTGATTAATCATGCTAGCTGTTTCC 2280
Db 2182 TTGTTCCCTTTTATGAGGTTTAAATTTTCAGCTTGGGCTGATTAATCATGCTAGCTGTTTCC 2241
QY 2281 TGTGTGAAATTTGTTATCCGCTCAAAATTTCCACACATACGAGCCGGAGGACATAAAGTG 2340
Db 2242 TGTGTGAAATTTGTTATCCGCTCAAAATTTCCACACATACGAGCCGGAGGACATAAAGTG 2301

QY	1321	AGCCTCCCGACCTGCGCCTTACGACTACGGCGCCTTGAACTCACAATCAACGCGCAGATC	1380
Db	1321	TGGA-CGCGCGCAGCCCGGGTGACCGCGTGTCTCTTCCGGCAGCTTGCGCCCGC	1379
QY	1381	ATGCAGTGCACACACAGCAAGCACACGCGGCCTACGTGAACAACCTGAACGTCCAGG	1440
Db	1380	GCCAAGCTCAGCGCTTCTTCGCGCTTGAGGGCTTCCGACCGAGCGGAACAGCTCC-AG	1438
QY	1441	GAGAAGTACAGGAGGGCTTGGCCAGAGGAGATGTTACAGCCACAGATAGCTTTCAGCCT	1500
Db	1439	CCGGCCCATCCAAGTGCACAGTTCGGGACCTGAGCCAGGGCTGCGAGTCCACCGGGC	1498
QY	1501	GCACCTGAAGTTCAATGTGTGTGTGCATCAATCATATAGCATTTTCTGGACAACACTCAGC	1560
Db	1499	CCACTCAACCCCGCTGGCG-----TGCCGCAACCCGCGC	1533
QY	1561	CCTAACGGTGTGAGAACCAAGGGAGTGTCTGGAAGCCATCAAAAGTACTTTGGT	1620
Db	1534	ACCGGGCGACTTCGGCAACTTCGCGTCCGACCGCAGCCTCTGGAGGTACCGCGCG	1593
QY	1621	TCCTTTGACAAAGTTTAAAGGAGACTGACGGCTGCATCTGTGTGTCTCAAGGCTCAGGT	1680
Db	1594	GCCT-----GGCGCCTCGCTCGCGGCCCGCACTCCATC	1628
QY	1681	TGGGGTTGGCTTGTTCATATAGGAAGGGGACACTTACAAATTGCTGTTCNAAT	1740
Db	1629	GTGGCGGGCGC-----TGSGTGTCCACGCTGGCGGAGACACCTGGCGCGCG	1678
QY	1741	CAGGATCCACTGCAAGGAACAACAGGCTTATTCACCTGTGGGGATGTGATGTGGGAG	1800
Db	1679	CGGCACACGCGCAGCTGGAGACG-----GGAAACGCGGCGC	1717
QY	1801	CACGCTTACTACCTTCAGTATAAAATGTCAAGCCTGATTAATCTAAAGCTATTTGGAAT	1860
Db	1718	CGCGTGGCTGTCTCGTGTGGCGTGTGGCGCGCGGCTCTGGGAGCGCCAGCGCG	1777
QY	1861	GTAATCAACTGGGAGATGTAACTGAAGATACATGCTTGCACAAAGTAAACACAGAT	1920
Db	1778	GGAGCACTCAGAGCGCAAGAGCGCGCGCGAGAGAGCTGCAAGCGCGCTGAAAGCT	1837
QY	1921	CGTTATGCTGGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANA	1980
Db	1838	TGATATCG-----	1845
QY	1981	AAAAACGGAATTCCTCCAGCCGGGGATCCACTAGTTCCTAGAGCGCGCCACCGCG	2040
Db	1846	-----AATTCTCGACCCGGGGATCCACTAGTTCCTAGAGCGCGCCACCGCG	1895
QY	2041	GTGGAGCTCCACACTAGAACTGCAAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGC	2100
Db	1896	GTGGAGCTCCACACTAGATGCAAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGC	1955
QY	2101	TATTCGCTTATTTGTAACATTAAGCTGCAATTAACAAGTTTAACAACATTCGATCA	2160
Db	1956	TATTCGCTTATTTGTAACATTAAGCTGCAATTAACAAGTTTAACAACATTCGATCA	2015
QY	2161	TTTTATGTTTCAGGTTTCAGGGGAGTGTGGAGGTTTTTAAAGCCACAGCTCCAGCTT	2220
Db	2016	TTTTATGTTTCAGGTTTCAGGGGAGTGTGGAGGTTTTTAAAGCCACAGCTCCAGCTT	2075
QY	2221	TTGTTCCCTTTAGTGAGGGTTAATTTTCAGCTTGGCGTAAATCATGCTCATAGCTGTTTCC	2280
Db	2076	TTGTTCCCTTTAGTGAGGGTTAATTTTCAGCTTGGCGTAAATCATGCTCATAGCTGTTTCC	2135
QY	2281	TGTGTGAATTTGTTATCGCTCACAAATTCACAAACATACGAGCGGAAGCATAAAGTG	2340
Db	2136	TGTGTGAATTTGTTATCGCTCACAAATTCACAAACATACGAGCGGAAGCATAAAGTG	2195
QY	2341	TAAAGCCTGGGTGCTTAATGAGTGAGCTTAACTCACTAATTTGCGTTTGGCGTCACTGCC	2400
Db	2196	TAAAGCCTGGGTGCTTAATGAGTGAGCTTAACTCACTAATTTGCGTTTGGCGTCACTGCC	2255
QY	2401	CGCTTTCCAGTCCGGAACCTGTGTGCGAGCTGCATTAATTAATTCGCGCAACCGCGCGG	2460
Db	2256	CGCTTTCCAGTCCGGAACCTGTGTGCGAGCTGCATTAATTAATTCGCGCAACCGCGCGG	2315
QY	2461	GAGAGCGGTTTGGCTATTTGGCGCTCTTCGCGCTTCCTCGCTCACTGACTCGCTGCGCTC	2520
Db	2316	GAGAGCGGTTTGGCTATTTGGCGCTCTTCGCGCTTCCTCGCTCACTGACTCGCTGCGCTC	2375
QY	2521	GCTGCTTCGGCTTCGCGGAGCGGTATCAGTCACTCAAAAGGGGTAAATACGGTTATCCAC	2580
Db	2376	GCTGCTTCGGCTTCGCGGAGCGGTATCAGTCACTCAAAAGGGGTAAATACGGTTATCCAC	2435
QY	2581	AGAATCAGGGATACGACGAGGAAGAAACATGTGACAAAAGCCAGCAAAAGGCCAGGAA	2640
Db	2436	AGAATCAGGGATACGACGAGGAAGAAACATGTGACAAAAGCCAGCAAAAGGCCAGGAA	2495
QY	2641	CGGTAAAAAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCGCGCCCCCTGACGAGCATCA	2700
Db	2496	CGGTAAAAAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCGCGCCCCCTGACGAGCATCA	2555
QY	2701	CAAAAATCGACGCTCAAGTTCAGAGTGGCGGAACCGGACAGACTATAAAGATACACGC	2760
Db	2556	CAAAAATCGACGCTCAAGTTCAGAGTGGCGGAACCGGACAGACTATAAAGATACACGC	2615
QY	2761	GTTCCTCCCTGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCTCTGCGCTTACCGGATA	2820
Db	2616	GTTCCTCCCTGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCTCTGCGCTTACCGGATA	2675
QY	2821	CTGTGCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACTGTTAGGTA	2880
Db	2676	CTGTGCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACTGTTAGGTA	2735
QY	2881	TCCTCAGTTCGCTGTAGTTCGCTTCCAAAGTTCGGCTGTGTGACAGAACCCCGCTTCA	2940
Db	2736	TCCTCAGTTCGCTGTAGTTCGCTTCCAAAGTTCGGCTGTGTGACAGAACCCCGCTTCA	2795
QY	2941	GCCGACCGCTCGGCTTATCCGCTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGCACGA	3000
Db	2796	GCCGACCGCTCGGCTTATCCGCTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGCACGA	2855
QY	3001	CTTATCGCACTGGGAGCAGCCACTGTTAAACAGGATTAAGCAGCGAGGTATGTAGCGCG	3060
Db	2856	CTTATCGCACTGGGAGCAGCCACTGTTAAACAGGATTAAGCAGCGAGGTATGTAGCGCG	2915
QY	3061	TGCTACAGAGTTCCTTCAAGTGTGGCTAACTACGCTACACTAGAGGACAGTATTTGG	3120
Db	2916	TGCTACAGAGTTCCTTCAAGTGTGGCTAACTACGCTACACTAGAGGACAGTATTTGG	2975
QY	3121	TATTCGCTCTGCTCAAGCCAGTTACCTTCGGAAGAGTTGGTAGCTCTTGATCCCG	3180
Db	2976	TATTCGCTCTGCTCAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCTTGATCCCG	3035
QY	3181	CAAAACAAACACCGCTGTAGCGGTGTTTTTTTGTTCGAAAGCAGATTACGCGCAG	3240
Db	3036	CAAAACAAACACCGCTGTAGCGGTGTTTTTTTGTTCGAAAGCAGATTACGCGCAG	3095
QY	3241	AAAAAAGGATTCACAAAGAGTCTTTTGTATCGGGTCTGACGCTCAGTGGAA	3300
Db</			

Db 3336 ATT CAGAAGAACTCGTCAAGAGCGGATAGAGGCGATGCGTCGAATCGGAGCGCG 3395
Qy 3541 ATACCGTAAAGCAGGAGGAGCGGTACGCCATTCGCGGCAAGCTCTTACGACATATCA 3600
Db 3396 ATACCGTAAAGCAGGAGGAGCGGTACGCCATTCGCGGCAAGCTCTTACGACATATCA 3455
Qy 3601 CGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATG 3660
Db 3456 CGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATG 3515
Qy 3661 AATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGAGGATCGCCATGGTC 3720
Db 3516 AATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGAGGATCGCCATGGTC 3575
Qy 3721 ACAGCAGATCTCTCGCGTGGGCGATCGCTCGCTTGGAGCGCTGGCGACAGTTCGGCTGGC 3780
Db 3576 ACAGCAGATCTCTCGCGTGGGCGATCGCTCGCTTGGAGCGCTGGCGACAGTTCGGCTGGC 3635
Qy 3781 GCGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAGACCGGCTTCCATCCGA 3840
Db 3636 GCGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAGACCGGCTTCCATCCGA 3695
Qy 3841 GTACGCTCTGCTCGATGCGATGTTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGATCA 3900
Db 3696 GTACGCTCTGCTCGATGCGATGTTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGATCA 3755
Qy 3901 AGCGTATGACGCGCCGATTCGATCAGCATGATGATGATGATGATGATGATGATGATGATG 3960
Db 3756 AGCGTATGACGCGCCGATTCGATCAGCATGATGATGATGATGATGATGATGATGATGATG 3815
Qy 3961 TGAGATGACAGGAGATCTCTGCGCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCT 4020
Db 3816 TGAGATGACAGGAGATCTCTGCGCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCT 3875
Qy 4021 TCAGTGAACAGTTCGACGACAGTTCGCGCAAGGAAACCGCCGTCGTGGCCAGCCAGTATG 4080
Db 3876 TCAGTGAACAGTTCGACGACAGTTCGCGCAAGGAAACCGCCGTCGTGGCCAGCCAGTATG 3935
Qy 4081 CGCGCTCGCTCTGCTTCAGTTCATTCCAGGCGACCGGACAGGTCGCTTTCGACAAAGA 4140
Db 3936 CGCGCTCGCTCTGCTTCAGTTCATTCCAGGCGACCGGACAGGTCGCTTTCGACAAAGA 3995
Qy 4141 ACCGGCGCCCTCGCTGCTGACGCGGAAACACGCGCGCATCAGAGCAGCGATGCTCTGT 4200
Db 3996 ACCGGCGCCCTCGCTGCTGACGCGGAAACACGCGCGCATCAGAGCAGCGATGCTCTGT 4055
Qy 4201 TGTGCCAGTATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAAT 4260
Db 4056 TGTGCCAGTATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAAT 4115
Qy 4261 CCATCTTGTTCATATGCGAAACGATCCTCATCTCTCTTGTATCAGAGCTTGATCCC 4320
Db 4116 CCATCTTGTTCATATGCGAAACGATCCTCATCTCTCTTGTATCAGAGCTTGATCCC 4175
Qy 4321 CTGCGCCATCAG 4332
Db 4176 CTGCGCCATCAG 4187

RESULT 4

ADT55139

ID ADT55139 standard; DNA; 4058 BP.

XX AC ADT55139;

XX AC ADT55139;

DT 30-DEC-2004 (first entry)

XX Nucleotide sequene of expression vector pMB1-hlFNalpha.

XX Ophthalmologic; radiation; free radical; superoxide anion;

KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;

KW glutathione peroxidase 4; GPX-4; gamma glutamyl transpeptidase;

KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
XX psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
OS Homo sapiens.
OS Simian virus 40.
OS Synthetic.

PH Key Location/Qualifiers
FT intron 332..497.
FT /tag= a
FT /note= "human beta-globin intron"
FT polyA_signal 347..503
FT /tag= b
FT /note= "SV40 late gene polyadenylation signal"
FT promoter 471..1162
FT /tag= c
FT /note= "CMV promoter"
FT CDS 551..1077
FT /tag= d
FT /note= "human interferon (IFN) alpha cDNA"
FT rep_origin 1158..1825
FT /tag= e
FT /note= "ColE1 ori from pBluescript SK+"
FT CDS 1226..2020
FT /tag= f
FT /gene= "kanamycin resistance gene"

XX WO2004087873-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009194.

XX 26-MAR-2003; 2003US-0458793P.

XX 25-MAR-2004; 2004US-0777889.

XX (GENT-) GENTERIC INC.

XX Bennett MJ, Chen Y;

XX WPI; 2004-737685/72.

XX Attenuating increases in concentrations of radiation-induced free

PT radicals in a mammalian cell, comprises contacting the cell with one or

PT more nucleic acids encoding proteins that neutralizes or eliminates a

PT portion of free radicals.

XX Claim 34; SEQ ID NO 5; 58pp; English.

XX The specification describes a method for attenuating increases in

CC concentrations of radiation-induced free radicals, superoxide anions or

CC heavy metal cations in a mammalian cell. The method comprises contacting

CC the cell with one or more nucleic acids encoding one or more proteins

CC that are expressed in the cell and that neutralizes or eliminates a

CC portion of the free radicals, superoxide anions or heavy metal cations in

CC the cell. The proteins are selected from metallothionein, superoxide

CC dismutase, catalase, glutathione peroxidase (GPX)-4, or gamma glutamyl

CC transpeptidase. The method is useful for attenuating increases in

CC concentrations of radiation-induced free radicals, superoxide anions or

CC heavy metal cations in a mammalian cell, and ameliorating symptoms of

CC xerostomia or xerophthalmia associated with conditions such as autoimmune

CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus

CC erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic

CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,

CC hepatitis C, cancer and decrease in mastication. The present sequence

CC represents an expression vector used in the method of the invention to

CC express the relevant proteins.

XX Sequence 4058 BP; 999 A; 1038 C; 1051 G; 970 T; 0 U; 0 Other;

Query Match 72.7%; Score 3147.8; DB 13; Length 4058;

Best Local Similarity 85.6%; Pred.No. 0;		Matches 3710; Conservative 0; Mismatches 348; Indels 274; Gaps 8;	
Qy	1	CGGTGGGGGCTCTTCGCTATTACGCGAGCTGCGAAAGGGGGAATGTCTGCAAGCGAT	60
Db	1	CGGTGGGGGCTCTTCGCTATTACGCGAGCTGCGAAAGGGGGAATGTCTGCAAGCGAT	60
Qy	61	TAAATGGGTAAAGCCAGCGGTTTCCAGTCAAGCTTGTAAACGAGCGCCAGTGAAT	120
Db	61	TAAATGGGTAAAGCCAGCGGTTTCCAGTCAAGCTTGTAAACGAGCGCCAGTGAAT	120
Qy	121	TGTAATACGACTCACTATAGGGGAAATGGGTACTGGCCACAGAGCTTGCGCCATTGCAAT	180
Db	121	TGTAATACGACTCACTATAGGGGAAATGGGTACTGGCCACAGAGCTTGCGCCATTGCAAT	180
Qy	181	ACGTTGATCCATATCAATAATGTATATTTATTTATTTGGCTCATGTCTCAACATTTACCGCCA	240
Db	181	ACGTTGATCCATATCAATAATGTATATTTATTTATTTGGCTCATGTCTCAACATTTACCGCCA	240
Qy	241	TGTTGACATTTGATTTAGCTAGTATTATATAGTAATCAATTACGGGGTCATTAGTTTCAT	300
Db	241	TGTTGACATTTGATTTAGCTAGTATTATATAGTAATCAATTACGGGGTCATTAGTTTCAT	300
Qy	301	AGCCATATATGGAGTTCCCGTTTACATAACTTACGGTAAATGGCCGCGCTGCTGACCG	360
Db	301	AGCCATATATGGAGTTCCCGTTTACATAACTTACGGTAAATGGCCGCGCTGCTGACCG	360
Qy	361	CCGAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAAACGCCAATA	420
Db	361	CCGAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAAACGCCAATA	420
Qy	421	GGGACTTTTCAATTGACGTCGAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCAGTA	480
Db	421	GGGACTTTTCAATTGACGTCGAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCAGTA	480
Qy	481	CATCAAGTGATATATGCCAAGTACGCCCGCTTATTTGACGTCAATGACGTAATGGCCCC	540
Db	481	CATCAAGTGATATATGCCAAGTACGCCCGCTTATTTGACGTCAATGACGTAATGGCCCC	540
Qy	541	GCCTGGCATATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTAC	600
Db	541	GCCTGGCATATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTAC	600
Qy	601	GTATTAGTCATCGCTATTACCATGGTCAATCGGTTTTGGCAGTACATCAATGGCGTGA	660
Db	601	GTATTAGTCATCGCTATTACCATGGTCAATCGGTTTTGGCAGTACATCAATGGCGTGA	660
Qy	661	TAGCGGTTTGACTCAACGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTG	720
Db	661	TAGCGGTTTGACTCAACGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTG	720
Qy	721	TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCTAACTCCGCCCATTTGACG	780
Db	721	TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCTAACTCCGCCCATTTGACG	780
Qy	781	CAAAATGGCGGTAGCGGTGACGTTGAGAGTCTATATAGCAGAGCTCGTTTAGTGAAC	840
Db	781	CAAAATGGCGGTAGCGGTGACGTTGAGAGTCTATATAGCAGAGCTCGTTTAGTGAAC	840
Qy	841	CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAGACACCGGGAC	900
Db	841	CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAGACACCGGGAC	900
Qy	901	CGATCCAGCCTGACTCTTAGCCTAGCTCTGAAGTTTGGTGGGCGCTTGGGAGGTTGGT	960
Db	901	CGATCCAGCCTGACTCTTAGCCTAGCTCTGAAGTTTGGTGGGCGCTTGGGAGGTTGGT	960
Qy	961	ATCAAGGTTACAGACAGGTTTAAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGA	1020
Db	961	ATCAAGGTTACAGACAGGTTTAAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGA	1020
Qy	1021	AGACTCTTTGGGTTTCTGATAGGCACATGACTCTCTCTGCTTATTTGGTCTATTTTCCCAACC	1080

Db	1021	AGACTCTTGGGTTTCTGATAGCACTGACTCTCTCTGCTCTATTGGTCTATTATTTCCACACC	1081
Qy	1081	TTAGGCTGCTGGTCTGAGCCTTAGGAGATCTCTCGAGGTCGACGGTATTCGATTAAGCTTGAAT	1140
Db	1081	TTAGGCTGCTGGTCTGAGCCTTAGGAGATCTCTCGAGGTCGACGGTATTCGATTAAGCTTGAAT	1140
Qy	1141	ATCGAATTCGGGCGGCGCAGGACGGCACTCGTGGCTGCTGTGGCTTCGGCAGGCGCTT	1200
Db	1141	ATCACAGAGAGACCAATGACCTTTGACTGTTGGCTCTCTCTGGTCTCTCTGGTGC-----	1195
Qy	1201	CAGCAGATCGGCGCATACGCGGTAGCACAGCAGCAGTACGAGCATGTTGAGCCGGCGAGTG	1260
Db	1196	-----TCAGCTCAAGTCAAGCTGCTCTCTGGCTGTGATCTG	1233
Qy	1261	TGCGGCACCAAGCAGGACGCTGGCTCGGTTTTGGGGTATCTCGGCTCCAGGCAGAGCAC	1320
Db	1234	CCTCAAAACCCACAG-----CCTGGGTAGCAGGAGGACCTTGG	1269
Qy	1321	AGCCTCCGACCTGCCCTACGACTACGGCGCCTGGAACTCACATCAACGCGCAGATC	1380
Db	1270	ATGCTCTTGCCACAG-----ATGAGGAGAAATC	1296
Qy	1381	ATCGAGTGCACACACAGCAAGCACACGCGGCTCTAGTGAAACAACTGAACTCACCGAG	1440
Db	1297	TCTCTTTTCTCTGCTTGAAGGACAGACATGACTTTGGATTTCCCGCAGGAGGATTTGGC	1356
Qy	1441	GAGAAGTACCAGGAGCGTTGGCCAAAGGGAGATGTTACAGCCCCAGATAGCTCTTCAGCCT	1500
Db	1357	AACAGTTCCAAAGGCTGAACCA-----	1381
Qy	1501	GCATGAAAGTTCAATGGTGGTGTGATATCAATCATAGCATTTTTCTGGGCAAAACCTCAGC	1560
Db	1382	-----TCCCTGCTCCATGAGATGATCCAGCAGATCTTCAAT	1419
Qy	1561	CCTAACGGTGTGGGAAACCAAGGGGAGTCTCTGMAAGCCATCAAACTGACTTTGGT	1620
Db	1420	CTCTTCAGCAACAAGGACTCATCTGCTGTTGGATGAGACCTCTTAGACAATTTCTAC	1479
Qy	1621	TCCTTTGACAAGTTTAAGGAGAAAGCTGACGGCTGCGATCTGTTGGTGTCCAAAGCTCAGGT	1680
Db	1480	ACTGAATCTTACAGCAGCTGAATGACTCTGGAAGCCTGTGT-----GATACAGGGGGT	1532
Qy	1681	TGGGTGGCTTGGTTTCAATAGGAACGGGACACTTACAAATGCTGCTTGTCCCAAT	1740
Db	1533	GGGGGTGACAGAGACTCCCTGTATGAAGGAGGACTC-----	1568
Qy	1741	CAGGATCCACTGCAAGGAACAAACAGGCTTTATTCCACTGCTGGGGATGATGTGTGGAG	1800
Db	1569	-----CATTTGCTGTGAGGAAATACTTCCAAAGA	1599
Qy	1801	CAGCTTACTACCTTCAGTTTAAAAATGTCAGGCTGATTTACTTAAAGCTATTTGAAT	1860
Db	1600	ATCACTCTCTATCTGAAGAAGAAATAACAGCCCTTGTCCCTGGGAGGTGTACAGACA	1659
Qy	1861	GTAATCAACTGGGAGAAATGTACTGAAAGATACATGGCTTGCAAAAGATAAACACCAAT	1920
Db	1660	GAATCA-----TGAGAT	1672
Qy	1921	CGTTATGCTGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1980
Db	1673	CTTTTTCTTTGTCACAAACTTGCAAGAAAGTTTAAAGATTAAGAAATGAATCTGGTTC	1732
Qy	1981	AAAAACGGAATTCCTGCAGCCCGGGGATCCACTAGTTCTAGAGCGGCGCCACCGCG	2040
Db	1733	AA-----CATTGAATAGCTGAGCGCGCCACCGCG	1766
Qy	2041	GTGGAGCTCCAACTAGAATGCAGTGAATAAATAATGCTTTATTGTGAAATTTGTGATGC	2100
Db	1767	GTGGAGCTCCAACTAGAATGCAGTGAATAAATAATGCTTTATTGTGAAATTTGTGATGC	1826
Qy	2101	TATTGCTTTATTGTAAACCATTAAGCTGCAATAAACAGTTTAACCAATTCGATTC	2160
Db	1827	TATTGCTTTATTGTAAACCATTAAGCTGCAATAAACAGTTTAACCAATTCGATTC	1886


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Db      4047 CTGGCCATCAG 4058
|||||
RESULT 5
ADT55137
ID      ADT55137 standard; DNA; 5753 BP.
XX
AC      ADT55137;
XX
DT      30-DEC-2004 (first entry)
XX
DE      Nucleotide sequene of expression vector pMB1-Catalase.
XX
KW      Ophthalmological; radiation; free radical; superoxide anion;
KW      heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
KW      glutathione peroxidase 4; Gpx-4; gamma glutamyl transpeptidase;
KW      xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW      graft-versus-host disease; systemic lupus erythematosus;
KW      rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW      psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
XX
OS      Homo sapiens.
OS      Simian virus 40.
OS      Synthetic.
XX
FH      Key
CDS     Location/Qualifiers
FT      11..2270
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FT      /note= "human catalase cDNA"
FT      332..497
FT      /*tag= b
FT      /note= "human beta-globin intron"
FT      347..503
FT      /*tag= c
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PN      WO2004087873-A2.
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PD      14-OCT-2004.
XX
PF      26-MAR-2004; 2004WO-US009194.
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PR      26-MAR-2003; 2003US-0458793P.
PR      25-MAR-2004; 2004US-07778889.
XX
PA      (GENT-) GENTERIC INC.
XX
PI      Bennett MJ, Chen Y;
XX
WPI     2004-737685/72.
XX
PT      Attenuating increases in concentrations of radiation-induced free
PT      radicals in a mammalian cell, comprises contacting the cell with one or
PT      more nucleic acids encoding proteins that neutralizes or eliminates a
PT      portion of free radicals.
XX
PS      Claim 34; SEQ ID NO 3; 58pp; English.
XX
CC      The specification describes a method for attenuating increases in
CC      concentrations of radiation-induced free radicals, superoxide anions or
CC      heavy metal cations in a mammalian cell. The method comprises contacting
CC      the cell with one or more nucleic acids encoding one or more proteins
CC      that are expressed in the cell and that neutralizes or eliminates a

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CC portion of the free radicals, superoxide anions or heavy metal cations in the cell. The proteins are selected from metallothionein, superoxide dismutase, catalase, glutathione peroxidase (Gpx)-4, or gamma glutamyl transpeptidase. The method is useful for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell, and ameliorating symptoms of xerostomia or xerophthalmia associated with conditions such as autoimmune disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic dysfunction, conditions affecting the CNS, psychogenic disorder, trauma, hepatitis C, cancer and decrease in mastication. The present sequence represents an expression vector used in the method of the invention to express the relevant proteins.

XX
SQ Sequence 5753 BP; 1479 A; 1416 C; 1418 G; 1440 T; 0 U; 0 Other;
Query Match 54.1%; Score 2341.8; DB 13; Length 5753;
Best Local Similarity 99.4%; Pred. No. 2.6e-248;
Matches 2349; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 1971 AAAAAAAAAAAAAACGGAAATCCCTGCAGCCCGGGGATCCACTAGTCTTAGAGCGGC 2030
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Qy 3392 ACAATAAATACTGTAGGAATTCCTGCAGCCCGGGGATCCACTAGTCTTAGAGCGGC 3451
Db |||||
Qy 2031 CGCCACCGGTGAGCTCCACAACACTAGATGCTGAAAAAATGCTTTATTTGTGAAA 2090
Db |||||
Qy 3452 CGCCACCGGTGAGCTCCACAACACTAGATGCTGAAAAAATGCTTTATTTGTGAAA 3511
Db |||||
Qy 2091 TTTGTGATGCTATTGCTTTATTTGTAACCAATTAAGCTGCAATAAACAAGTTAAACAACA 2150
Db |||||
Qy 3512 TTTGTGATGCTATTGCTTTATTTGTAACCAATTAAGCTGCAATAAACAAGTTAAACAACA 3571
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Qy 2151 ATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTTGAGGCTTTTAAAGCCACA 2210
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Qy 3572 ATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTTGAGGCTTTTAAAGCCACA 3631
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Qy 2211 GCTCCAGCTTTGTTCCCTTTAGTGCAGGTTAAATTCGAGCTTGCCTGTAATCATGTCAT 2270
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Qy 3632 GCTCCAGCTTTGTTCCCTTTAGTGCAGGTTAAATTCGAGCTTGCCTGTAATCATGTCAT 3691
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Qy 2271 AGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAATTCACACACATACGAGCCGAA 2330
Db |||||
Qy 3692 AGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAATTCACACACATACGAGCCGAA 3751
Db |||||
Qy 2331 GCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTTAATCATGTTGCTGTC 2390
Db |||||
Qy 3752 GCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTTAATCATGTTGCTGTC 3811
Db |||||
Qy 2391 GCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCAGCTGCATTAATGAATCGGCC 2450
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Qy 3812 GCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCAGCTGCATTAATGAATCGGCC 3871
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Qy 2451 AACGCGCGGGAGAGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACT 2510
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Qy 3872 AACGCGCGGGAGAGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACT 3931
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Qy 2511 CGCTCGGCTCGGTCGTTCCGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATAC 2570
Db |||||
Qy 3932 CGCTCGGCTCGGTCGTTCCGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATAC 3991
Db |||||
Qy 2571 GGTATTCACAGAATCAGGGGATAACGAGGAAAGCAATGTGAGCAAAAGGCCAGCAA 2630
Db |||||
Qy 3992 GGTATTCACAGAATCAGGGGATAACGAGGAAAGCAATGTGAGCAAAAGGCCAGCAA 4051
Db |||||
Qy 2631 AGGCCAGGAACCGTAAAAAGCGGTTGCTGGGCTTTTTCATAGGCTCCGCCCCCTG 2690
Db |||||
Qy 4052 AGGCCAGGAACCGTAAAAAGCGGTTGCTGGGCTTTTTCATAGGCTCCGCCCCCTG 4111
Db |||||
Qy 2691 ACAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAA 2750
Db |||||
Qy 4112 ACAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAA 4171
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CDS 1173..3419
 /*tag= f
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 CDS 1226..2020
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 WO2004087873-A2.
 14-OCT-2004.
 26-MAR-2004; 2004WO-US009194.
 26-MAR-2003; 2003US-0458793P.
 25-MAR-2004; 2004US-07778889.
 (GENT-) GENTERIC INC.
 Bennett MJ, Chen Y;
 WPI; 2004-737685/72.
 Attenuating increases in concentrations of radiation-induced free radicals in a mammalian cell, comprises contacting the cell with one or more nucleic acids encoding proteins that neutralizes or eliminates a portion of free radicals.
 Claim 34; SEQ ID NO 4; 58pp; English.
 The specification describes a method for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell. The method comprises contacting the cell with one or more nucleic acids encoding one or more proteins that are expressed in the cell and that neutralizes or eliminates a portion of the free radicals, superoxide anions or heavy metal cations in the cell. The proteins are selected from metallothionein, superoxide dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl transpeptidase. The method is useful for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell, and ameliorating symptoms of xeroderma or xerophthalmia associated with conditions such as autoimmune disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic dysfunction, conditions affecting the CNS, psychogenic disorder, trauma, hepatitis C, cancer and decrease in mastication. The present sequence represents an expression vector used in the method of the invention to express the relevant proteins.
 SQ Sequence 5760 BP; 1471 A; 1422 C; 1426 G; 1441 T; 0 U; 0 Other;
 Query Match 54.1%; Score 2341.8; DB 13; Length 5760;
 Best Local Similarity 99.4%; Pred. No. 2.6e-248;
 Matches 2349; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1971 AAAAAAAAAAAGGAAATCCCTCAGCCCGGGGATCCACTAGTCTTAGAGCGGC 2030
 DB 3399 ACAATAAATAATCTCTACGGAATCCTCGAGCCCGGGGATCCACTAGTCTTAGAGCGGC 3458
 QY 2031 CGCCACCGCGGTGAGCTCCCAACTAGAACTAGAGTGAAGAAATGCTTTATTTGTGAAA 2090
 DB 3459 CGCCACCGCGGTGAGCTCCCAACTAGAACTAGAGTGAAGAAATGCTTTATTTGTGAAA 3518
 QY 2091 TTTGTGATGCTATTGCTTTATTTGTAACCAATTATAGCTGCAATAAACAAGTTAAACA 2150
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 QY 2211 GCTCCAGCTTTTGTCCCTTTATAGTGAAGGTTAAATTCGAGCTTGGCGTAAATCATGTGAT 2270
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QY 2271 AGCTGTTTCTGTGTAATTTGTTATCCGCTCAAAATTCACACAAATACAGACCGGAA 2330
 DB 3699 AGCTGTTTCTGTGTAATTTGTTATCCGCTCAAAATTCACACAAATACAGACCGGAA 3758
 QY 2331 GCATAAGTGTAAAGCCTGGGTGCTTAATAGTGAAGTAACTACATTAATTCGTTGC 2390
 DB 3759 GCATAAGTGTAAAGCCTGGGTGCTTAATAGTGAAGTAACTACATTAATTCGTTGC 3818
 QY 2391 GCTCACTGCCCGCTTTCCAGTTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC 2450
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 QY 2451 AAGCGCGGGGAGAGCGGTTTGGGTATTCGGGCTCTTCGGCTTCTCGCTCACTGACT 2510
 DB 3879 AAGCGCGGGGAGAGCGGTTTGGGTATTCGGGCTCTTCGGCTTCTCGCTCACTGACT 3938
 QY 2511 CGTCGCTCGCTCGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAGAGCGGTAATAC 2570
 DB 3939 CGTCGCTCGCTCGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAGAGCGGTAATAC 3998
 QY 2571 GGTATCCACAGATCAGGGGATTAACGACAGAAAGAAACATGTGAGCAAAAGCGCAGCAAA 2630
 DB 3999 GGTATCCACAGATCAGGGGATTAACGACAGAAAGAAACATGTGAGCAAAAGCGCAGCAAA 4058
 QY 2631 AGGCAGAAACCGTAAAGAGCGCGTTCGTCGGGTTCCTCATAGGCTCCGCCCCCTG 2690
 DB 4059 AGGCAGAAACCGTAAAGAGCGCGTTCGTCGGGTTCCTCATAGGCTCCGCCCCCTG 4118
 QY 2691 ACAGAGATCAAAAAATCGAGCTCAAGTCAGAGTGGCGGAGGAAACCCGACAGGACTATAA 2750
 DB 4119 ACAGAGATCAAAAAATCGAGCTCAAGTCAGAGTGGCGGAGGAAACCCGACAGGACTATAA 4178
 QY 2751 GATACACAGGCTTTCCCTCGGAAAGTCCCTCGTCGGCTTCCTGTTCCGACCTCGCCG 2810
 DB 4179 GATACACAGGCTTTCCCTCGGAAAGTCCCTCGTCGGCTTCCTGTTCCGACCTCGCCG 4238
 QY 2811 TTACCGGATACCTTCGCGCTTCCTCGGAAAGGTCGCGCTTCTCAATGCTCAC 2870
 DB 4239 TTACCGGATACCTTCGCGCTTCCTCGGAAAGGTCGCGCTTCTCAATGCTCAC 4298
 QY 2871 GCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCCAGCTGGGCTGTGTGACGAAAC 2930
 DB 4299 GCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCCAGCTGGGCTGTGTGACGAAAC 4358
 QY 2931 CCCCCTTCAGCCGACCGCTTCGCGCTTATCCGGTAACTATCGCTTTCAGTCCACCCGG 2990
 DB 4359 CCCCCTTCAGCCGACCGCTTCGCGCTTATCCGGTAACTATCGCTTTCAGTCCACCCGG 4418
 QY 2991 TAAGACAGCTTATCGCCACTGCGCAGCAGCACTGGTAAACAGGATTAAGCAGAGCGAGT 3050
 DB 4419 TAAGACAGCTTATCGCCACTGCGCAGCAGCACTGGTAAACAGGATTAAGCAGAGCGAGT 4478
 QY 3051 ATGTAGGCGGTGTACAGAGTTCCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAAGA 3110
 DB 4479 ATGTAGGCGGTGTACAGAGTTCCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAAGA 4538
 QY 3111 CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGTAGCT 3170
 DB 4539 CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGTAGCT 4598
 QY 3171 CTTGATCCGGCAAAACAAACCAACCGCTGCTAGCGGTGGTTTTTTTGTTCGAAGAGCAGA 3230
 DB 4599 CTTGATCCGGCAAAACAAACCAACCGCTGCTAGCGGTGGTTTTTTTGTTCGAAGAGCAGA 4658
 QY 3231 TTACCGCAGAAAAAAGATCTCAAGAGATCTCTTTGATCTTTTCTACGGGCTGTGAGC 3290
 DB 4659 TTACCGCAGAAAAAAGATCTCAAGAGATCTCTTTGATCTTTTCTACGGGCTGTGAGC 4718
 QY 3291 CTCAGTGGAAACGAAACCTCAGTTAAGGATTTTCGTATGAGCGATACATATTGAT 3350
 DB 4719 CTCAGTGGAAACGAAACCTCAGTTAAGGATTTTCGTATGAGCGATACATATTGAT 4778

Db 86 GACGTCAATATGACGTATGTTCCATAGTAACGCCAATAGGACCTTTCCATTGACGTCA 145
 Qy 441 ATGGGTGAGTATTTACGGTAAATGCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 500
 Db 146 ATGGGTGAGTATTTACGGTAAATGCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 205
 Qy 501 AAGTACGCCCTTATGACGTCAATGACGGTAAATGCGCCCTGGCAATATGCCAGTA 560
 Db 206 AAGTACGCCCTTATGACGTCAATGACGGTAAATGCGCCCTGGCAATATGCCAGTA 265
 Qy 561 CATGACCTTATGGACCTTTCTACTTGGCAGTAATCTACGTATAGTATCGCTATTTAC 620
 Db 266 CATGACCTTATGGACCTTTCTACTTGGCAGTAATCTACGTATAGTATCGCTATTTAC 325
 Qy 621 CATGGTATGGGTTTTGGCAGTACATCAATGGGGTGGATAGCGTTTGAAGTACACGGG 680
 Db 326 CATGGTATGGGTTTTGGCAGTACATCAATGGGGTGGATAGCGTTTGAAGTACACGGG 385
 Qy 681 ATTTCCAAAGTCTCCACCCCAATGACGTCAATGGGAGTTTGTGGCACCAAAATCAACG 740
 Db 386 ATTTCCAAAGTCTCCACCCCAATGACGTCAATGGGAGTTTGTGGCACCAAAATCAACG 445
 Qy 741 GGAATTTCCAAATGCTGTAAACAACTCCGCCCAATGACGCAATATGGCGGTAGCGTGT 800
 Db 446 GGAATTTCCAAATGCTGTAAACAACTCCGCCCAATGACGCAATATGGCGGTAGCGTGT 505
 Qy 801 ACGTGGGAGTCTATATAGCAGAGCTCGTTTGTAGTGAACGCTGAGATCGCTGGAGACG 860
 Db 506 ACGTGGGAGTCTATATAGCAGAGCTCGTTTGTAGTGAACGCTGAGATCGCTGGAGACG 565
 Qy 861 CCATCCACGCTGTTTGTACCTCCATAGAGACACCGGGACCGATCCAGCCTGACTCTAGC 920
 Db 566 CCATCCACGCTGTTTGTACCTCCATAGAGACACCGGGACCGATCCAGCCTCCGGGCGG 625
 Qy 921 CTAGCTCTGAAGTGGTGGTAGGCCCTCGGGCAGGTGGTATCAAGTTACAGACAGGT 980
 Db 626 GGAACGGTGCATTGGAACGCG----- 646
 Qy 981 TTAAGGAGACCAATAGAACTGGGCATGTGGAGACAGAGACACTTTGGGTTCTGTGATA 1040
 Db 647 -----GATTCGCCGTGTTAATTAACAGGTAGTGTCTTCTCCTGTTTCC 691
 Qy 1041 GGCACCTGACTCTCTGCTGCTATGTTCTATTTTCCACCCCTTAGCGTCTGGTCTGAGCC 1100
 Db 692 TTCCCTCTGCTATTTCTGCTCAACCTTCTCATAGAACTGCAGTATCTGTATTTGCTAG 751
 Qy 1101 TAGGAGATCTCTGAGGTGACGGTATCGATAAGCTTGNATCGAATTCGGGGCGGCA 1160
 Db 752 CAGTAATACTAACGGTTCTTTTCTCTTCAAGGCCACCAAGCTTCCATGGGGTGGC 811
 Qy 1161 GGAGCGGCACTGTGCTGTGGTCTCGGACGGGCTTCAGCAGATCGGGGCATCAG 1220
 Db 812 CGAACGCCCCACCTGCTGCTGCTCTCCTGCTGCTGATCTCTCTGGGCTCCAGT 871
 Qy 1221 CGGTAGCACAGCACTAGCAGCATGTTGAGCCGGCAGTGTGCGGCACAGCAGGAGCT 1280
 Db 872 CCTCTGTGCTCCCCACCGCTCATCTCGACAGTCTGGGTGCTGGAGAGGTACATCTGGA 931
 Qy 1281 GGTCCGGTTTTGGGGTATCTGGGCTCAGGCGAGACAGCCTCCCGACCTCCCTTA 1340
 Db 932 GGCCAAAG-----AGGCAGAAAATGTCAAGATGGGTTGTGAGAA 971
 Qy 1341 CGACTACGGCGGCTCGAACTCACAATCAACGGCGCAGATCATGCACTGCACACAGCAA 1400
 Db 972 GGTCCAGACTGAGTGAAA----- 990
 Qy 1401 GCACCAAGCGGCTACTAGTGAACAACTGAACTGACCGAGGAGAACTACAGAGCGGTT 1460
 Db 991 --ATATTACAGTCCACAGATACCAAAAGTCAACTTCTATGCTTGGAAAAGAAATGGAGGTGA 1048
 Qy 1461 GGCCAGGGAGATGTTACAGCCAGATAGCTCTTACGGCTGCACTCAAGTTCAATGGTGG 1520

Db 1049 AGAACAGG-----CCATCGAAGTGTGGCAAGGCCCTGTCCCTGCTCAGCGAAGCCATCCTGC 1104
 Qy 1521 TGGTCAATCAATCATAGCAATTTTCTGGACAAACCTCAGCCCTAAACGGTGGTGAGAAC 1580
 Db 1105 AGCCCAAGCCCTGCTGGCCAAATTTCTCCAGCCACAGAGACCCCTCAGCTGCATATCG 1164
 Qy 1581 CAAAGGGGAGTGTGTGAAGCCATCAAAACGTGACTTTGGTTCCTTTGACAAAGTTAAGGA 1640
 Db 1165 ACRAAGCCATCAGTGGTCTGC----- 1185
 Qy 1641 GAGCTGACGGCTGCATCTGTGTGTGTCCAAGGCTCAGGTTGGGGTTGGCTGTGTTTCAA 1700
 Db 1186 -----GCAGGCTCACTTCCCTGCTGCGGGTGTCTGGAGCTCAG 1223
 Qy 1701 TAAGGAACGGGACACTTACAAATTTGCTGTGTTGCCAAATCAGGATCCATGCAAGGAAC 1760
 Db 1224 AAGGAATGTATGTCCTCCAT----- 1247
 Qy 1761 AACAGGCTTATTTCCACTGCTGGGATGTATGTGTGGGACGCTTACTTACCTTCAGTA 1820
 Db 1248 -----ACCACCCCACTGCTCCACTTCC 1269
 Qy 1821 TAAAAATGTCAAGGCTGATTTCTAAAAGCTATTTGGAATGTAATCAACTGGGAGAAATG 1880
 Db 1270 GCACACTCAGTGGATATCTTCTGCAAGCTCTTCCGGGTCTAGCCCA----- 1317
 Qy 1881 TAAGTAAGATACATGGCTTGCAAAAGTAAACCCAGATCGTTTATGCTGGAATAAAAAA 1940
 Db 1318 -----ACTTCTCCGGGGAAACTGAAGCTGTACACGGGAGAGGTCTG 1360
 Qy 1941 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2000
 Db 1361 CAGGAGAGGGACAGGTGAGTC-----TAGAAAAGCCGAATTTCTGCAGG 1404
 Qy 2001 GCCCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCGGTGGAGCTTCCACAACAGAA 2060
 Db 1405 AATTGGGTGGCATCCCTGTGACCCCTCCCAGTGCCTCTCTGCGCCCTGGAGTTGCCAC 1464
 Qy 2061 TGCAGTAAAAAATGCTTATTTGTGAAATTTGTGATGCTTATGCTTATTTATTTAAACA 2120
 Db 1465 TCCAGTCCCAACAGCCCTTGTCTTAATAAATAAATTAAGTTGCATCATTTTGTCTGACTAGT 1524
 Qy 2121 TTATAAGCTGCAATAAACAAGTTAAACAATTTGATTCATTTTATGTTTTCAGGTTTCAGG 2180
 Db 1525 GTCTTCTATATATATATGCGGTGGAGGGGGTGTATGGAGCAAGGGCAGTTGGGAA 1584
 Qy 2181 GGGAGGTGTGGAGGTTTTTTAAAGCCACAGCTCCAGCTTTTGTTCCTTTAGTACAGGT 2240
 Db 1585 GACAACCTGTAGGGCTCGAGGGGGGCGCGGTACCAGCTTTTGTTCCTTTAGTACAGGT 1644
 Qy 2241 TAAATTCAGCTTGGCGTAATCATGGTCAATAGCTGTTTCTGTGTGAAATTTGTTATCCGC 2300
 Db 1645 TAAATTCAGCTTGGCGTAATCATGGTCAATAGCTGTTTCTGTGTGAAATTTGTTATCCGC 1704
 Qy 2301 TCACAAATTCACACAACTACAGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAAAT 2360
 Db 1705 TCACAAATTCACACAACTACAGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAAAT 1764
 Qy 2361 GAGTACAGTAACTCACTTAAATTTGCGTTCAGCTCAGTCCCGCTTTTCCAGTCGGGAAAC 2420
 Db 1765 GAGTACAGTAACTCACTTAAATTTGCGTTCAGTCCCGCTTTTCCAGTCGGGAAAC 1824
 Qy 2421 TGTGTGCGAGTGCATTAATGAATCGGCAACCGCGGGAGAGCGGTTTTCGCTATG 2480
 Db 1825 TGTGTGCGAGTGCATTAATGAATCGGCAACCGCGGGAGAGCGGTTTTCGCTATG 1884
 Qy 2481 GCGCTCTTTCGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2540
 Db 1885 GCGCTCTTTCGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 1944
 Qy 2541 CGGTATCAGCTCACTCAAAAGCGGTAAATACCGTTATTCACAGAAATCAGGGGATTAACGAG 2600
 Db 1945 CGGTATCAGCTCACTCAAAAGCGGTAAATACCGTTATTCACAGAAATCAGGGGATTAACGAG 2004

Qy	2601	GAAGAAATGTCAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGCGGTTC	2660
Db	2005	GAAGAAATGTCAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGCGGTTC	2064
Qy	2661	TGGCGTTTTCATAGAGCTCGCCCGCTGACGAGCATCAAAAATCGACGCTCAAGTC	2720
Db	2065	TGGCGTTTTCATAGAGCTCGCCCGCTGACGAGCATCAAAAATCGACGCTCAAGTC	2124
Qy	2721	AGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGGCTTTCCCGCTGGAGCTCC	2780
Db	2125	AGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGGCTTTCCCGCTGGAGCTCC	2184
Qy	2781	TCGTGCGCTCTCTGTTCCGACCTCGCCTTACCGGATACCTGTCCGCTTTCTCCCTT	2840
Db	2185	TCGTGCGCTCTCTGTTCCGACCTCGCCTTACCGGATACCTGTCCGCTTTCTCCCTT	2244
Qy	2841	CGGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTAGTGC	2900
Db	2245	CGGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTAGTGC	2304
Qy	2901	TTGCTCTCAAGCTGGGCTGTTGTCACGAAACCCCGCTTACGCGCAGCGCTGGCCTTAT	2960
Db	2305	TTGCTCTCAAGCTGGGCTGTTGTCACGAAACCCCGCTTACGCGCAGCGCTGGCCTTAT	2364
Qy	2961	CCGTTAACTATCGTCTTGGTTCGAACCCGTTAAGACACGACTTATCGCCACTGGCAGCAG	3020
Db	2365	CCGTTAACTATCGTCTTGGTTCGAACCCGTTAAGACACGACTTATCGCCACTGGCAGCAG	2424
Qy	3021	CCACTGTAAAGGATTTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTTCTGAAGT	3080
Db	2425	CCACTGTAAAGGATTTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTTCTGAAGT	2484
Qy	3081	GCTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTCGCTCTCTGTAAGC	3140
Db	2485	GCTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTCGCTCTCTGTAAGC	2544
Qy	3141	CAGTTACCTTCGGAAAAAGTTGGTAGCTCTTTGATCCGGCAAAACCAACCGCTGGTA	3200
Db	2545	CAGTTACCTTCGGAAAAAGTTGGTAGCTCTTTGATCCGGCAAAACCAACCGCTGGTA	2604
Qy	3201	CGCGTGGTTTTTTTGTGACGAGCAGATTAGCGCAGAAAAAAGGATCTCAGAAG	3260
Db	2605	CGCGTGGTTTTTTTGTGACGAGCAGATTAGCGCAGAAAAAAGGATCTCAGAAG	2664
Qy	3261	ATCCTTTGATCTTTTCTACGGGTCTCAGCGTCAGTGCAGAAACTCAGCTTAAGGA	3320
Db	2665	ATCCTTTGATCTTTTCTACGGGTCTCAGCG	2695
Qy	3321	TTTTGGTCAATGACGGATACATATTTGAATGTATTTAGAAAAATAAACAATAGGGGTT	3380
Db	2696	-----	2695
Qy	3381	CGCGCACATTTCCCGAAAGTGCCACCTGTATGCGGTGTGAATACCGCACAGATGCGT	3440
Db	2696	-----	2695
Qy	3441	AAGGAGAAAAATACCGCATCAGAAATTTGAAGGTTAATAATTCAGAAAGACTCGTCAAG	3500
Db	2696	-----TCAGNAGAACTCGTCAAG	2713
Qy	3501	AAGCGGATAGAAGCGATGCGTTCGGAATCGGAGCGCGGATACCGTTAAAGCACAGGAA	3560
Db	2714	AAGCGGATAGAAGCGATGCGTTCGGAATCGGAGCGCGGATACCGTTAAAGCACAGGAA	2773
Qy	3561	CGCGTACGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGGATACCGCAACCGCTATGC	3620
Db	2774	CGCGTACGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGGATACCGCAACCGCTATGC	2833
Qy	3621	CTGATAGCGGTCCGCCACACCCAGCGGCCACAGTTCGATGAATCCAGAAAGCGGCATT	3680
Db	2834	CTGATAGCGGTCCGCCACACCCAGCGGCCACAGTTCGATGAATCCAGAAAGCGGCATT	2893
Qy	3681	TTCCACCATGATATTCCGCAAGCAGCGATCGCCATGGGTCAACGAGATCTTCGCCGTC	3740
Db	2894	TTCCACCATGATATTCCGCAAGCAGCGATCGCCATGGGTCAACGAGATCTTCGCCGTC	2953
Qy	3741	GGGATGCTCGCTTGGAGCTTGGCGAACAGTTTCGGCTTGGCGAGCCCTTGATGCTTTC	3800
Db	2954	GGGATGCTCGCTTGGAGCTTGGCGAACAGTTTCGGCTTGGCGAGCCCTTGATGCTTTC	3013
Qy	3801	GTCCAGATCATCTGATCGACAAAGCCGCTTCCATCCGAGTACGTCGCTCGATGCG	3860
Db	3014	GTCCAGATCATCTGATCGACAAAGCCGCTTCCATCCGAGTACGTCGCTCGATGCG	3073
Qy	3861	ATGTTTTCGCTTGGTGTGCAATGGGAGGTAGCCGATCAAGGTTATGACGCCCGCAT	3920
Db	3074	ATGTTTTCGCTTGGTGTGCAATGGGAGGTAGCCGATCAAGGTTATGACGCCCGCAT	3133
Qy	3921	TGCATCAGCATGATGATACCTTTCTCGGAGAGCAAGTGATGATGACAGGATCTCTG	3980
Db	3134	TGCATCAGCATGATGATACCTTTCTCGGAGAGCAAGTGATGATGACAGGATCTCTG	3193
Qy	3981	CCCAGGACCTTCCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAAGTGAACAGTTCGAC	4040
Db	3194	CCCAGGACCTTCCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAAGTGAACAGTTCGAC	3253
Qy	4041	AGCTGCGCAAGGAACCCCGTCTGTGGCCAGCCAGTACGCGCTGCTTCTTGCAG	4100
Db	3254	AGCTGCGCAAGGAACCCCGTCTGTGGCCAGCCAGTACGCGCTGCTTCTTGCAG	3313
Qy	4101	TTCAATTCAGGACCCGAGCAGGTCGCTTCTTGACAAAAGAACCCGGGGCCCTTGCCTGA	4160
Db	3314	TTCAATTCAGGACCCGAGCAGGTCGCTTCTTGACAAAAGAACCCGGGGCCCTTGCCTGA	3373
Qy	4161	CAGCCGGAACACCGCGGCATCAGAGCAGCGATTGTCTGTGTGCCAGTCATAGCCGAA	4220
Db	3374	CAGCCGGAACACCGCGGCATCAGAGCAGCGATTGTCTGTGTGCCAGTCATAGCCGAA	3433
Qy	4221	TAGCTCTCCACCCAAAGCCGAGAACCTGCGTGCAATCCATCTTGTTCATCATGCG	4280
Db	3434	TAGCTCTCCACCCAAAGCCGAGAACCTGCGTGCAATCCATCTTGTTCATCATGCG	3493
Qy	4281	AAACGATCTCATCTCTCTTGTATCAGAGTTGATCCCTGCGGCATCAG	4332
Db	3494	AAACGATCTCATCTCTCTTGTATCAGATCTTGTATCCCTGCGGCATCAG	3545
RESULT 8			
ID	AAI70084	standard; DNA; 3589 BP.	
XX	AAI70084;		
AC	AC		
XX	XX		
DT	11-SEP-2003 (revised)		
DT	21-DEC-2001 (first entry)		
XX	XX		
DE	Plasmid pIF0921 encoding human interferon-alpha.		
XX	XX		
KW	Plasmid pIF0921; interferon-alpha; cytokine; human; gene delivery;		
KW	immune disorder; gene therapy; vaccine; ds.		
XX	XX		
OS	Homo sapiens.		
OS	Human herpesvirus 5.		
XX	Chimeric.		
XX	XX		
PH	Key	Location/Qualifiers	
FT	768..1334		
FT	/*tag= a		
FT	/product= "human interferon-alpha"		
XX	XX		
PN	W0200166149-A2.		
XX	XX		
PD	13-SEP-2001.		
XX	XX		
PF	02-MAR-2001; 2001WO-US006953.		

1231	AGAGAAATACAGCCCTTGTCCCTGGGGAGGTGTGCAGAGCAGAAATCATGAGATCTTTTT	1299
QY	GTAACTGAAGATACATGGCTTGC AAAAAGTAAACCGATCGTTATGCTGGAAAAAAA	1939
DB	CTTTGTC-----A	1298
QY	AAACGGATTCCTCGC	1999
DB	AAAGATCTGACAG	1358
QY	AGCCGGGGATCCACTAGTTCTTAGAGCGCGCCACCGCGSGTGGAGCTCCACAACCTAGA	2059
DB	GAATTGGGTGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTCGCCCTGGAAGTGC	1418
QY	ATGCAGTGA AAAAATGCTTTATTTGTGAATTTGTGATGCTATGTCTTTATTTGTGA	2119
DB	CTCAGTGC CCACAGCGCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTG	1478
QY	ATTATAAGCTCAATAAACAAAGTTAAACAAATTGCAATCATTTATTTGTTTCAG	2179
DB	TGTCCTCTATAATATTATGCGGTGGAGGGGTGGTATGGAGCAAGGCGCAAGTTGG	1538
QY	GGGAGGTGTGGAGGTTTTTAAAGCCACAGCTCCAGCTTTTGTTCCTTTTGTGAGGG	2239
DB	AGACAACCTGTAGGGCTCGAGGGGGGCGCGGTACACAGCTTTTGTTCCTTTTGTG	1598
QY	TTAATTTGAGCTTTGGCGTAAATCATGTGCATAGCTGTTCTCTGTGCAAAATGTT	2299
DB	TTAATTTGAGCTTTGGCGTAAATCATGTGTCATGTCTTCTGTGTGAAAATTTGT	1658
QY	CTCAAAATCCACAACAATACGAGCGCGGAGCAATAAGTGTAAAGCTCGGGGTGC	2359
DB	CTCAAAATCCACAACAATACGAGCGCGGAGCATAAAGTGTAAAGCTCGGGGTGC	1718
QY	TGAGTGAGCTAACTCACATTAATTTGCGTTGGCTCACTGCGCGTTTCCAGT	2419
DB	TGAGTGAGCTAACTCACATTAATTTGCGTTGGCTCACTGCGCGTTTCCAGT	1778
QY	CTGTGTCGCCAGCTGCATTAATGAATCGGCCCAACCGCGCGGGAGAGCGGTTT	2479
DB	CTGTGTCGCCAGCTGCATTAATGAATCGGCCCAACCGCGCGGGAGAGCGGTTT	1838
QY	GGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGCG	2539
DB	GGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGCG	1898
QY	GCGGTATCAGCTCACTCAAAAGGCGTAAACGGTTATCCACAGAAATCAGGGG	2599
DB	GCGGTATCAGCTCACTCAAAAGGCGTAAACGGTTATCCACAGAAATCAGGGG	1958
QY	GGAAAGAACATGTGAGCAAAAGGCCACAAAGGCCAGGAACCGTAAAAAGGCGG	2659
DB	GGAAAGAACATGTGAGCAAAAGGCCACAAAGGCCAGGAACCGTAAAAAGGCGG	2018
QY	CTGGCGTTTTCATAGCTTCGCGCCCGCTGACGAGCATCACAAAATCAGCGCT	2719
DB	CTGGCGTTTTCATAGCTTCGCGCCCGCTGACGAGCATCACAAAATCAGCGCT	2078
QY	CAGAGTGGGAAACCCGACAGGACTATAAGATACCAAGCGCTTCCCGCTGGA	2779
DB	CAGAGTGGGAAACCCGACAGGACTATAAGATACCAAGCGCTTCCCGCTGGA	2138
QY	CTGTGCGCTCTCTGTTCGGAACCTGCGCGTTACCGGATACCTGTCCGCTTTC	2839
DB	CTGTGCGCTCTCTGTTCGGAACCTGCGCGTTACCGGATACCTGTCCGCTTTC	2198
QY	TCGGGAAGCGTGGCGCTTCTCAATGTCTCAGCTGTAGGTATCTCAGTTTCG	2899
DB	TCGGGAAGCGTGGCGCTTCTCAATGTCTCAGCTGTAGGTATCTCAGTTTCG	2258
QY	GTTCGCTCCAGCTGGGCTGTGTGCAGAAACCCCGCTTCAGCCGACCGCTGC	2959
DB	GTTCGCTCCAGCTGGGCTGTGTGCAGAAACCCCGCTTCAGCCGACCGCTGC	2318

Db 989 AACCAT----- 994
Qy 1521 TGGTCATATCAATCATAGCATTTTCTGGACAAACCTCAGCCCTAACCGTGGTGAGAAC 1580
Db 995 ---CCCTGTCTCCATGATGATGATCCAGCAGATCTTCAATCTTTCAGCACAAGAGGACTC 1051
Qy 1581 CAAGGGGAGTTGCTGGAGGCATCAACAGTGACTTTTGGTTCTTTTGACAAAGTTTAAAGGA 1640
Db 1052 ATCTGCTGTTGGGATGAGACCTCTAGACAAATTTCACTGAACTTACAGAGAGCT 1111
Qy 1641 GAAGCTGACGGCTGATCTGTGTGTCTCAAGGCTCAGGTTGGGTTGGCTTGTGTTCAA 1700
Db 1112 GAATCAGCTGGAAGCCTGTG-----GATACAGGGGTTGGGTTGACAGAGACTCCCC 1164
Qy 1701 TAAGGAAGGGGACACTTACAAATTTGCTGTGTTGTTCCAAATCAGGATCCACTGCAAGGAC 1760
Db 1165 TGATGAAGGAGGACTC----- 1180
Qy 1761 AACAGGCTTATTCACACTGCTGGGATGATGTGTGGAGCAGCTTACTACTTTCAGTA 1820
Db 1181 -----CATCTGGCTGTGAGGAATACTTCCAAAGATCACTCTCTATCTGAAGA 1231
Qy 1821 TAAAAATGTGAGGCTGATATCTAAAGCTATTTGGAATGTAATCAACTGGGGAGAAATG 1880
Db 1232 GAAGAAATACAGCCCTTGTGCTGGAGGTTGTGAGAGCAGAAATCATGAGATCTTTTTC 1291
Qy 1881 TAACTGAAGATACATGGCTTGCAAAAGTAAGTAACCAAGTCGTTATGCTGGAAGAAAAA 1940
Db 1292 TTTGT-----CAA 1299
Qy 1941 AAAAAAIAA 2000
Db 1300 CAAACTTGCAGAAAGTTTAAAGATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1359
Qy 2001 GCCCGGGGATCCATGATTTAGAGGCGCCCAAGCGGCTGAGCTCCACAATAGAA 2060
Db 1360 AATTGGGTGGCATCCCTGTGACCCCTCCCAAGTCCCTCTCTGCGCCCTGGAAGTTGCCAC 1419
Qy 2061 TGCAAGTGAIAAATATTTTATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTA 2120
Db 1420 TCCAGTCCCAACCAAGCTTTGCTTAATAAATTAAGTTGCAATTTGTTGCTGACTAGGT 1479
Qy 2121 TTATAAGCTGCAATAAACAAGTTAAACAATTCATTTTATTTATTTGTTTTCAGGTTTCAGG 2180
Db 1480 GTCCTTCTATAATATTATGGGTGGAGGGGTGATGGAGCAAGGGCAAGTTGGGA 1539
Qy 2181 GGGAGGTGTGGAGGTTTTTAAAGCCACAGCTCCAGCTTTTGTTCCTTTTGTAGGAGGT 2240
Db 1540 GACAACTGTAGGGCTCGAGGGGGGGCCCGGTACAGCTTTTGTTCCTTTTGTAGGAGGT 1599
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Db 1600 TAATTTTCAGCTTCGGCTTAATCATGCTCATAGCTGTTTCTGCTGAAATTTGTTATCCGC 1659
Qy 2301 TCACAATTTCCACACAATACAGAGCCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTAAT 2360
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Qy 2361 GAGTGAGCTAACTACATTAATTCGGTTGGCTCAGTCCCGCTTTCAGTCGGGAACC 2420
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Qy 2421 TGTGCTGCAGCTGCAATTAATGAATCGGCCAAAGCGGGGAGAGGGGTTTGGGTATTG 2480
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Qy 2481 GGCCTCTTCGGTTCTCGCTCATGCTGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2540
Db 1840 GGCCTCTTCGGTTCTCGCTCATGCTGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 1899
Qy 2541 CGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCAGATCAGGGGATTAACGCGAG 2600

Db 1900 CGGTATCAGCTCACTCAAGCGCGTAAATACGGTTATCCACAGATCAGGGGATAACGCGAG 1959
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Db 1960 GAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAACCGTAAAGAGCCCGCTTGC 2019
Qy 2661 TGGCGTTTTTCCATAGGCTCGGCCCTCAGCAGCATCAAAAAATTCAGCGCTCAAGTC 2720
Db 2020 TGGCGTTTTTCCATAGGCTCGGCCCTCAGCAGCATCAAAAAATTCAGCGCTCAAGTC 2079
Qy 2721 AGAGGTGGCAAAACCCGACAGGACTATAAGATACAGGCGTTTCCCTTGGAAAGCTCCC 2780
Db 2080 AGAGGTGGCAAAACCCGACAGGACTATAAGATACAGGCGTTTCCCTTGGAAAGCTCCC 2139
Qy 2781 TCGTGGCTCTCTGTTTCCGACCTCGGCTTACCGGATACCTGTGCGCCTTCTCCCTT 2840
Db 2140 TCGTGGCTCTCTGTTTCCGACCTCGGCTTACCGGATACCTGTGCGCCTTCTCCCTT 2199
Qy 2841 CGGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGGTGCG 2900
Db 2200 CGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGGTGCG 2259
Qy 2901 TTCGCTCAAGCTGGGCTGTGCAAGAACCCCGCTTCAGCCCGAAGCGTGCSCCTTAT 2960
Db 2260 TTCGCTCAAGCTGGGCTGTGCAAGAACCCCGCTTCAGCCCGAAGCGTGCSCCTTAT 2319
Qy 2961 CCGGTAACTATCTGTTGAGTCCAAACCGGTAAAGACAGCACTTATCCCACTTGGCAGCGAG 3020
Db 2320 CCGGTAACTATCTGTTGAGTCCAAACCGGTAAAGACAGCACTTATCCCACTTGGCAGCGAG 2379
Qy 3021 CCACTGTTAAACAGGATTTAGCAGAGCGAGGTATGTAGGCGGTGCTTACAGAGTTCTTGAAGT 3080
Db 2380 CCACTGTTAAACAGGATTTAGCAGAGCGAGGTATGTAGGCGGTGCTTACAGAGTTCTTGAAGT 2439
Qy 3081 GGTGGCTAACTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGC 3140
Db 2440 GGTGGCTAACTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGC 2499
Qy 3141 CAGTTACTTTCGGAAAAAGAGTTGGTAGCTTTCATCCGGCAACCAACCAACCGCTGTA 3200
Db 2500 CAGTTACTTTCGGAAAAAGAGTTGGTAGCTTTCATCCGGCAACCAACCAACCGCTGTA 2559
Qy 3201 CGCGTGGTTTTTGTGCAAGCAGAGATTACGCGCAGAAAAAGGATCTCAAGAG 3260
Db 2560 CGCGTGGTTTTTGTGCAAGCAGAGATTACGCGCAGAAAAAGGATCTCAAGAG 2619
Qy 3261 ATCTTTGATCTTTTCTACGGGTCTGACCGCTCAGTGGAAAGAACTCAGTTAAGGGA 3320
Db 2620 ATCTTTGATCTTTTCTACGGGTCTGACCG----- 2650
Qy 3321 TTTTGGTTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAATAGGGGTTC 3380
Db 2651 ----- 2650
Qy 3381 CGCGCATTTTCCCGAAAAAGTCCACTGTATGCGGTGTGAATAATACCGCAGATCGGT 3440
Db 2651 ----- 2650
Qy 3441 AAGGAGAAATAACCGCATCAGGAAATTTGAAGCGTTAATAATTCAGAAAGTCTCGTCAAG 3500
Db 2651 -----TCAGAAAGTCTCGTCAAG 2668
Qy 3501 AAGCGCATAGAAAGCGATGCGTCCGAATCGGAGCGGCGATACCGTAAAGCAGAGGAA 3560
Db 2669 AAGCGCATAGAAAGCGATGCGTCCGAATCGGAGCGGCGATACCGTAAAGCAGAGGAA 2728
Qy 3561 GCGGTGAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGATACCGCAACCGTATGTC 3620
Db 2729 GCGGTGAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGATACCGCAACCGTATGTC 2788
Qy 3621 CTGATAGCGGTGCGGCACACCGGCGGCGCAGTGGATGAATCCAGAAAGCGGCCATT 3680
Db 2789 CTGATAGCGGTGCGGCACACCGGCGGCGCAGTGGATGAATCCAGAAAGCGGCCATT 2848

QY 3681 TTCCACCATGATATTTCGCAAGCAGGCGATCCCATGGTTCACAGCAGAGATCCTCGCGTC 3740
 DB |||||
 QY 2849 TTCCACCATGATATTTCGCAAGCAGGCGATCCCATGGTTCACAGCAGAGATCCTCGCGTC 2908
 DB |||||
 QY 3741 GGGCATGCTCCCTTGAGCCTGGCGAACAGATTCGGCTGGCGCGAGCCCTGATGCTCTTC 3800
 DB |||||
 QY 2909 GGGCATGCGCGCTTGAGCCTGGCGAACAGATTCGGCTGGCGCGAGCCCTGATGCTCTTC 2968
 DB |||||
 QY 3801 GTCCAGATCATCTTCATGCAAGACCGCTTCATCCGAGTACGTGCTGCTCGATGCG 3860
 DB |||||
 QY 2969 GTCCAGATCATCTTCATGCAAGACCGCTTCATCCGAGTACGTGCTGCTCGATGCG 3028
 DB |||||
 QY 3861 ATGTTTCGCTTGGTGGTTCGATGGCGAGTACCGGATCAAGCGTATGACGCCCGCAT 3920
 DB |||||
 QY 3029 ATGTTTCGCTTGGTGGTTCGATGGCGAGTACCGGATCAAGCGTATGACGCCCGCAT 3088
 DB |||||
 QY 3921 TGCAATCAGCCATGATGGATATCTTTCCTGGCGAGGCAAGGTGAGATGACAGGATCTCTG 3980
 DB |||||
 QY 3089 TGCAATCAGCCATGATGGATATCTTTCCTGGCGAGGCAAGGTGAGATGACAGGATCTCTG 3148
 DB |||||
 QY 3981 CCCCGGCACTTCGCGCAATAGCAGCGCTTCCTTCCTCCGCTTCAGTGACAAAGTGCAGCAC 4040
 DB |||||
 QY 3149 CCCCGGCACTTCGCGCAATAGCAGCGCTTCCTTCCTCCGCTTCAGTGACAAAGTGCAGCAC 3208
 DB |||||
 QY 4041 AGCTGCGCAAGGAACGCGCGTCTGGCCAGGACGATAGCGCGCTGCTCTCTTCGAG 4100
 DB |||||
 QY 3209 AGCTGCGCAAGGAACGCGCGTCTGGCCAGGACGATAGCGCGCTGCTCTCTTCGAG 3268
 DB |||||
 QY 4101 TTCAATCAGGCAACGCGACAGTTCGGTCTTGACAAAGAAAGACCGCGCGCTTCGCTGA 4160
 DB |||||
 QY 3269 TTCAATCAGGCAACGCGACAGTTCGGTCTTGACAAAGAAAGACCGCGCGCTTCGCTGA 3328
 DB |||||
 QY 4161 CAGCGGAACACGCGGCGATCAGACGCGGATTCGTTGTGCGCCAGTCAATAGCGGAA 4220
 DB |||||
 QY 3329 CAGCGGAACACGCGGCGATCAGACGCGGATTCGTTGTGCGCCAGTCAATAGCGGAA 3388
 DB |||||
 QY 4221 TAGCCTCTCCACCCAAAGCGCGGAGAACCTGCGTGCAATCCATCTTGTTCATCATCGG 4280
 DB |||||
 QY 3389 TAGCCTCTCCACCCAAAGCGCGGAGAACCTGCGTGCAATCCATCTTGTTCATCATCGG 3448
 DB |||||
 QY 4281 AAACGATCTCATCTCTCTCTTGTATCAGAGCTTGCATCCCTGCGCCATCAG 4332
 DB |||||
 QY 3449 AAACGATCTCATCTCTCTCTTGTATCAGAGCTTGCATCCCTGCGCCATCAG 3500
 DB |||||

RESULT 10
 ADF77242
 ID ADF77242 standard; DNA; 3589 BP.
 XX
 AC ADF77242;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human IPN pIF0921.
 XX
 KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US2003181405-A1.
 XX
 PD 25-SEP-2003.
 XX
 PF 29-APR-2002; 2002US-00136837.
 XX
 XX 12-MAR-1999; 99US-00268135.
 XX
 PA (NORD/) NORDSTROM J L.
 PA (PERI/) PERICLE F.
 PA (ROLL/) ROLLAND A.
 PA (RALS/) RALSTON R O.

XX Nordstrom JL, Pericle F, Rolland A, Ralston RO;
 PI WPI; 2004-020834/02.
 XX
 PT A mammalian interferon alpha expression plasmid is useful in gene therapy
 PT to deliver interferon alpha to cells to modulate tumor activity in the
 PT treatment of cancer.
 XX
 PS Disclosure; SEQ ID NO 4; 65pp; English.
 XX
 CC The invention relates to a mammalian interferon alpha expression plasmid,
 CC comprising a promoter and a synthetic 5' intron transcriptionally linked
 CC with an interferon alpha coding sequence and a 3' untranslated region.
 CC The mammalian interferon alpha expression plasmid is useful for treating
 CC tumour growth. The present sequence is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 3589 BP; 832 A; 983 C; 933 G; 841 T; 0 U; 0 Other;
 Query Match 44.4%; Score 1923.8; DB 12; Length 3589;
 Best Local Similarity 72.2%; Pred. No. 1.6e-202;
 Matches 2897; Conservative 0; Mismatches 603; Indels 512; Gaps 10;
 QY 321 CGTTACATAAATTACGTTAAATGCGCCCTGGCTGACCGCCCAACGACCCCGCCCAT 380
 DB 1 CGTTACATAAATTACGTTAAATGCGCCCTGGCTGACCGCCCAACGACCCCGCCCAT 60
 QY 381 GACGTCAATATGATGATGTTCCCATAGTAACGCCAATAGGGACTTTTCCATTGACGTCA 440
 DB 61 GACGTCAATATGATGATGTTCCCATAGTAACGCCAATAGGGACTTTTCCATTGACGTCA 120
 QY 441 ATGGGTGAGATTTTACGGTAAACTGCGCACTTGGCAGTACATCAAGTGTATCATATGCC 500
 DB 121 ATGGGTGAGATTTTACGGTAAACTGCGCACTTGGCAGTACATCAAGTGTATCATATGCC 180
 QY 501 AAGTACGCGCCCTATTGACGTCAATGAGGTAAATGGCCCGCTGGCATTTATGCCAGTA 560
 DB 181 AAGTACGCGCCCTATTGACGTCAATGAGGTAAATGGCCCGCTGGCATTTATGCCAGTA 240
 QY 561 CATGACCTTATGGGACTTTTCTTACTTTGGCAGTACATCTACGTATTAGTTCATGCTATTAC 620
 DB 241 CATGACCTTATGGGACTTTTCTTACTTTGGCAGTACATCTACGTATTAGTTCATGCTATTAC 300
 QY 621 CATGATGATCGGTTTGGCAGTACATCAATGCGGCTGGATAGCGTTTGACTACGCGG 680
 DB 301 CATGATGATCGGTTTGGCAGTACATCAATGCGGCTGGATAGCGTTTGACTACGCGG 360
 QY 681 ATTTCCAAAGTCTCCACCCCATTTGAGTCAATGGGAGTTTGTGTTGGCACCCAAATCAACG 740
 DB 361 ATTTCCAAAGTCTCCACCCCATTTGAGTCAATGGGAGTTTGTGTTGGCACCCAAATCAACG 420
 QY 741 GGACTTTCCAAAATGCTGTAACAATCCGCGCCCATTTGACGCAATGGGCGTAGGCGTGT 800
 DB 421 GGACTTTCCAAAATGCTGTAACAATCCGCGCCCATTTGACGCAATGGGCGTAGGCGTGT 480
 QY 801 ACGTGGGAGGTCTATATAAGCAGAGTCTGTTAGTGAACCGTCAAGTCCCTGGAGAGC 860
 DB 481 ACGTGGGAGGTCTATATAAGCAGAGTCTGTTAGTGAACCGTCAAGTCCCTGGAGAGC 540
 QY 861 CCATCCAGCTGTTTGGACCTCCATAGAGACACCGGACCGATCCAGCTGACTCTAGC 920
 DB 541 CCATCCAGCTGTTTGGACCTCCATAGAGACACCGGACCGATCCAGC----- 589
 QY 921 CTAGCTCTGAAGTTCGTTGGTGGGCGCTGGGAGGTTCAGAGTTACAGGTTACAGAGGT 980
 DB 590 ---CTCGCGCGCGGAAACGGTGCATTGGAACGCGGATTCGCCCGTGTAAATAACAGGT 645
 QY 981 TTAAGGAGACCAATAGAAACTGGGCACTGTGGAGACAGAGAACTCTTGGTTCGTGATA 1040
 DB 646 ----- 645
 QY 1041 GGCACCTGACTCTCTCTGCTCTATTGGTCTATTTTCCACCCCTTAGGCTGCTGCTGAGCC 1100

QY 3261 ATCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAAGCAAACTCAGTTAAGGGA 3320
 DB |||
 QY 2620 ATCTTTGATCTTTTCTACGGGGTCTGAGC----- 2650
 DB |||
 QY 3321 TTTTGGTCATGAGCGGATACATATTTTGAATGATTTAGAAAAATAAACAATAGGGTTC 3380
 DB ----- 2650
 QY 3381 CGCGCACATTTCCCGAAAGTGCCACCTGTATGCGGTGTGAATATACCGCACAGATGCGT 3440
 DB ----- 2650
 QY 2651 ----- 2650
 DB |||
 QY 3441 AAGGAGAAAATACCGCATCAGGAAATTTGAAGCGTTAATAATTCAGAGAATACTCGTCAAG 3500
 DB -----TCAAGAAACTCGTCAAG 2668
 QY 3501 AAGCGATAGAGCGATCGCTCGGAATCGGAGCGGGATACCGTAAAGCAGAGGAA 3560
 DB |||
 QY 2669 AAGCGATAGAGCGATCGCTCGGAATCGGAGCGGGATACCGTAAAGCAGAGGAA 2728
 DB |||
 QY 3561 GCGGTACGCCATTCGCCCGCAAGCTCTTCAGCAATATCAGGGTAGCAACGCTATGTC 3620
 DB GCGGTACGCCATTCGCCCGCAAGCTCTTCAGCAATATCAGGGTAGCAACGCTATGTC 2788
 QY 3621 CTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCAGAAAAAGCGGCCATT 3680
 DB |||
 QY 2789 CTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCAGAAAAAGCGGCCATT 2848
 DB |||
 QY 3681 TTCCACCATGATTTCCGCAAGCAGCGATCGCCATCGGTACGACGAGATCTTCGCCGTC 3740
 DB |||
 QY 2849 TTCCACCATGATTTCCGCAAGCAGCGATCGCCATCGGTACGACGAGATCTTCGCCGTC 2908
 DB |||
 QY 3741 GGGCATGCTCGCTTGGCTGGCAACAGTTTCGGCTGGCGGAGCCCTGATGCTCTTC 3800
 DB GGGCATGCGGCTTGGCTGGCAACAGTTTCGGCTGGCGGAGCCCTGATGCTCTTC 2968
 QY 3801 GTCCAGATCATCTGATGCACAAAGACCGGTTCCATCCGAGTACGTCTCGTCTCATCGG 3860
 DB |||
 QY 2969 GTCCAGATCATCTGATGCACAAAGACCGGCTTCCATCCGAGTACGTCTCGTCTCATCGG 3028
 DB |||
 QY 3861 ATGTTTCGGTGGTGGTCAATGGCAGCGTAGCGGATCAAGCGTATGACGCGCGCGAT 3920
 DB |||
 QY 3029 ATGTTTCGGTGGTGGTCAATGGCAGCGTAGCGGATCAAGCGTATGACGCGCGCGAT 3088
 DB |||
 QY 3921 TGCATCAGCATGATGGATACCTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTG 3980
 DB TGCATCAGCATGATGGATACCTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTG 3148
 QY 3981 CCCCAGCATTCGCCCAATAGCAGCGATCCCTTCCCGTTTCAAGTGAACAGCTCGAGCAC 4040
 DB |||
 QY 3149 CCCCAGCATTCGCCCAATAGCAGCGATCCCTTCCCGTTTCAAGTGAACAGCTCGAGCAC 3208
 DB |||
 QY 4041 AGCTGGCAAGGAACCGCGTCTGTCGACGACGATACCGGCTCGCTCTTTCGAG 4100
 DB |||
 QY 3209 AGCTGGCAAGGAACCGCGTCTGTCGACGACGATACCGGCTCGCTCTTTCGAG 3268
 DB |||
 QY 4101 TTTATTTCAGGACCGGACAGGTCTGTTTGAACAAAGAACCGGGCGCCCTTGGCTGA 4160
 DB |||
 QY 3269 TTTATTTCAGGACCGGACAGGTCTGTTTGAACAAAGAACCGGGCGCCCTTGGCTGA 3328
 DB |||
 QY 4161 CAGCGGAACACGGCGGATCAGAGCAGCGATGTTCTGTTGTCGAGTCAATAGCGGA 4220
 DB |||
 QY 3329 CAGCGGAACACGGCGGATCAGAGCAGCGATGTTCTGTTGTCGAGTCAATAGCGGA 3388
 DB |||
 QY 4221 TAGCCTCTCACCAAGCGGCGGAGAACCTGGTGCATTCATCTTTTCAATCATCGG 4280
 DB |||
 QY 3389 TAGCCTCTCACCAAGCGGCGGAGAACCTGGTGCATTCATCTTTTCAATCATCGG 3448
 DB |||
 QY 4281 AAACGATCTCTATCTCTTTGATCAGAGCTTGATCCCTTCGCGCATCAG 4332
 DB |||
 QY 3449 AAACGATCTCTATCTCTTTGATCAGATCTTGATCCCTTCGCGCATCAG 3500
 DB |||

RESULT 11
 ID AAA15565 standard; DNA; 8349 BP.
 XX AAA15565;
 AC AAA15565;
 XX 28-JUL-2000 (first entry)
 XX pMON30464 plasmid.
 XX Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran;
 KW Lepidopteran; Dipteran; plasmid transit peptide; zmsSU PTP; insecticidal;
 KW plasmid targeting peptide; pMON30464 plasmid; expression vector; ds.
 XX Synthetic.
 XX WO200026371-A1.
 XX 11-MAY-2000.
 XX 04-NOV-1999; 99WO-US026086.
 XX 04-NOV-1998; 98US-00186002.
 XX (MONS) MONSANTO CO.
 XX Corbin DR, Romano CP;
 XX WPI; 2000-376130/32.
 XX New method of expressing insecticidal proteins in plants transformed with
 PT a Bacillus thuringiensis delta-endotoxin encoding gene resulting in
 PT effective control of susceptible target pests.
 XX Example 1; Page 96-99; 104pp; English.
 CC Bacillus thuringiensis produce delta-endotoxins during sporulation. These
 CC proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran
 CC larvae. An insect-resistant transgenic plant has been constructed which
 CC contains the delta-endotoxin cry2Ab gene. The present sequence would be
 CC used to transfer delta-endotoxin genes into plant cells and for
 CC subsequent high expression of the cry2Ab gene. Protection may be attained
 CC against insects such as Ostrina spp., Diatraea spp., Helicoverpa spp.,
 CC and Spodoptera spp., in Zea mays; Heliothis virescens, Helicoverpa spp.,
 CC Pectinophora spp., in Gossypium hirsutum; Anticarsa spp., Pseudoplusia
 CC spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza
 CC sativa. Expression of the endotoxin by a plant cell produces a fusion
 CC protein comprising an amino-terminal plastid transit peptide (zmsSU PTP)
 CC covalently linked to the delta-endotoxin. The fusion protein functions to
 CC localise the delta-endotoxin to a subcellular organelle or compartment
 XX Sequence 8349 BP; 1959 A; 2355 C; 2088 G; 1947 T; 0 U; 0 Other;
 SQ Query Match 42.6%; Score 1845.4; DB 3; Length 8349;
 Best Local Similarity 92.6%; Pred. No. 5e-194;
 Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;
 QY 2249 AGCTTGGCGTAAATCAGTCAAGTCTGTTTCTGTTGAAATGTTATCCGCTCAAAAT 2308
 DB |||
 QY 5909 AGCTTGGCGTAAATCAGTCAAGTCTGTTTCTGTTGAAATGTTATCCGCTCAAAAT 5968
 DB |||
 QY 2309 CCACACACATACGAGCGCGAGCATAAAGTCTGAGGCTGCTTAATGAGTGAGC 2368
 DB |||
 QY 5969 CCACACACATACGAGCGCGAGCATAAAGTCTGAGGCTGCTTAATGAGTGAGC 6028
 DB |||
 QY 2369 TAACTCACATTAATTCGTTTGGCTTCCAGTCCCGCTTTTCCAGTCCGGAACCTGTCGTC 2428
 DB |||
 QY 6029 TAACTCACATTAATTCGTTTGGCTTCCAGTCCCGCTTTTCCAGTCCGGAACCTGTCGTC 6088
 DB |||
 QY 2429 CAGCTGCATTAATGAATCGGCCAAACGCGCGGAGAGCGGTTTGGGTATTTGGGCGCTCT 2488
 DB |||
 QY 6089 CAGCTGCATTAATGAATCGGCCAAACGCGCGGAGAGCGGTTTGGGTATTTGGGCGCTCT 6148
 DB |||


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Db 10486 ATTCGCGCCAGGCTCTTCAGCAATATACGGGTAGCCAAAGCTATGTCCTGATAGCGGT 10545
Qy 3632 CCGCCACACCCAGCGCGCCAGTCGATGATCCAGAAAGCGGCCATTTTCACCAATGA 3691
Db 10546 CCGCCACACCCAGCGCGCCAGTCGATGATCCAGAAAGCGGCCATTTTCACCAATGA 10605
Qy 3692 TATTGGCAAGCAGGATCGGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 3751
Db 10606 TATTGGCAAGCAGGATCGGCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 10665
Qy 3752 CTTGAGCTCGGCAACAGTTGCGTGGCGGAGCCCTGATGCTCTTTCGTCAGATCAT 3811
Db 10666 CTTGAGCTCGGCAACAGTTGCGTGGCGGAGCCCTGATGCTCTTTCGTCAGATCAT 10725
Qy 3812 CTTGATCGACAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCGATGCTTTCGCTT 3871
Db 10726 CTTGATCGACAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCGATGCTTTCGCTT 10785
Qy 3872 GGTGTCGAATGGGAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 3931
Db 10786 GGTGTCGAATGGGAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 10845
Qy 3932 TGATGATACCTTCTCGGACGAGCAGGATGAGATGACAGAGATCTCTGCGCGGACCTT 3991
Db 10846 TGATGATACCTTCTCGGACGAGCAGGATGAGATGACAGAGATCTCTGCGCGGACCTT 10905
Qy 3992 CGCCCAATAGCAGCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 4051
Db 10906 CGCCCAATAGCAGCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 10965
Qy 4052 GAACGCGCGTCTGCGGACGAGCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 4111
Db 10966 GAACGCGCGTCTGCGGACGAGCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 11025
Qy 4112 CACCGACAGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 4171
Db 11026 CACCGACAGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 11085
Qy 4172 CGCGGCGATCAGACGAGCAGGATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 4231
Db 11086 CGCGGCGATCAGACGAGCAGGATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 11145
Qy 4232 CCCAAGCGCGGAGAACCTCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 4291
Db 11146 CCCAAGCGCGGAGAACCTCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 11205
Qy 4292 ATCTGTCCTTGTATCAGAGCTTGATCCCTGCGGATCAG 4332
Db 11206 ATCTGTCCTTGTATCAGATCTTGATCCCTGCGGATCAG 11246

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RESULT 13

AAV50427 ID AAV50427 standard; DNA; 3600 BP.

AC AAV50427;

XX 26-OCT-1998 (first entry)

DE Plasmid pIG0552 upper expected sequence nucleotides 1-3600.

KW Human; IGF-1; insulin-like growth factor 1; urinary incontinence;

KW gene therapy; neurotrophic factor; ss.

OS Synthetic.

OS Homo sapiens.

FN W09833529-A1.

PD 06-AUG-1998.

XX 04-FEB-1998; 98WO-US002051.

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XX PR 04-FEB-1997; 97US-0036862P.
XX PA (GENE-) GENEMEDICINE INC.
XX PI Coleman M;
XX WPI; 1998-437184/37.
XX PT Treatment of urinary incontinence - by delivering nucleic acid vector for
XX expression of growth factor or neurotrophic factor in tissue(s).
XX PS Disclosure; Page 103-105; 117pp; English.
XX CC A method has been developed of treating urinary incontinence (UI) in
XX mammals. The method comprises delivering a nucleic acid vector for the
XX expression of a growth factor or neurotrophic factor in a tissue or
XX tissues. The present sequence represents the expected upper sequence of
XX plasmid pIG0552 nucleotides 1-3600 from the present invention. Due to the
XX growth and stimulatory effects of growth factors and neurotrophic
XX factors, introducing these factors to degenerated muscles in the urinary
XX system can improve UI by enhancing both their integrity and neural
XX innervation.
XX SQ Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;

Query Match 39.7%; Score 1719; DB 2; Length 3600;
Best Local Similarity 90.8%; Pred. No. 4.3e-180;
Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;

Qy 2214 CCAGCTTTTCTCCCTTTAGTGAGGGTTAATTCGAGCTTTGGCGTAATCATGTGCATAGC 2273
Db 20 CCAGCTTTTCTCCCTTTAGTGAGGGTTAATTCGAGCTTTGGCGTAATCATGTGCATAGC 79
Qy 2274 TGTTCCTGTGTGAATTTATCCGCTCAAAATTCACAAATACAGACGAGCCGGAAGCA 2333
Db 80 TGTTCCTGTGTGAATTTATCCGCTCAAAATTCACAAATACAGACGAGCCGGAAGCA 139
Qy 2334 TAAAGTGTAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGCTTGCCT 2393
Db 140 TAAAGTGTAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGCTTGCCT 199
Qy 2394 CACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCGAGCTGCATTAATGAATCGGCCAAC 2453
Db 200 CACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCGAGCTGCATTAATGAATCGGCCAAC 259
Qy 2454 GCGCGGGGAGAGCGGGTTTCGCTATTGGGCGCTCTTCGCTTCTCCTCACTGACTCGC 2513
Db 260 GCGCGGGGAGAGCGGGTTTCGCTATTGGGCGCTCTTCGCTTCTCCTCACTGACTCGC 319
Qy 2514 TGGCTCGGTCGTTCCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGT 2573
Db 320 TGGCTCGGTCGTTCCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGT 379
Qy 2574 TATCCACAGAAATCAGGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCGCAAAAGG 2633
Db 380 TATCCACAGAAATCAGGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCGCAAAAGG 439
Qy 2634 CCAGGACCGTAAAGGCGCGCTTCTGCTGGCTTTTCCATAGCTCCGCCCCCTGACG 2693
Db 440 CCAGGACCGTAAAGGCGCGCTTCTGCTGGCTTTTCCATAGCTCCGCCCCCTGACG 499
Qy 2694 AGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGGGAACCCGACAGGACTATAAAGAT 2753
Db 500 AGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGGGAACCCGACAGGACTATAAAGAT 559
Qy 2754 ACCAGCGTTTCCCTCTGGAAGCTCCCTCTGCGCTCTCTCTGTTCCGACCCCTGCGCTTA 2813
Db 560 ACCAGCGTTTCCCTCTGGAAGCTCCCTCTGCGCTCTCTCTGTTCCGACCCCTGCGCTTA 619
Qy 2814 CCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCAATGCTCAGCT 2873
Db 620 CCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCAATGCTCAGCT 679

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Qy 2874 GTAGTATCTCAGTTCGGTGTAGTTCGTTCCCAAGCTGGCTGTGTGACGAACCCC 2933
Db |||||||
Dy 680 GTAGTATCTCAGTTCGGTGTAGTTCGTTCCCAAGCTGGCTGTGTGACGAACCCC 739
Qy 2934 CCGTTACGCCGACCGCTGGCGCTTATCCGGTAACTATCGTTCGATTCGAACCGGTAA 2993
Dy |||||||
Dy 740 CCGTTACGCCGACCGCTGGCGCTTATCCGGTAACTATCGTTCGATTCGAACCGGTAA 799
Qy 2994 GACACGACTTATCGCACTGGCAGCAGCACTGGTAAACAGATTAGCAGACGAGGTATG 3053
Dy |||||||
Dy 800 GACACGACTTATCGCACTGGCAGCAGCACTGGTAAACAGATTAGCAGACGAGGTATG 859
Qy 3054 TAGCGGTGCTACAGAGTCTTTGAAGTGTGTGCTTAACCTACGGCTACACTAGAAGGACAG 3113
Dy |||||||
Dy 860 TAGCGGTGCTACAGAGTCTTTGAAGTGTGTGCTTAACCTACGGCTACACTAGAAGGACAG 919
Qy 3114 TATTTGGTATCTGGCTCTGCTGAAGCCAGTACCTTCGGAAAGAGATTGGTAGCTCTT 3173
Dy |||||||
Dy 920 TATTTGGTATCTGGCTCTGCTGAAGCCAGTACCTTCGGAAAGAGATTGGTAGCTCTT 979
Qy 3174 GATCCGGCAAAACAAACCAACCGCTGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTA 3233
Dy |||||||
Dy 980 GATCCGGCAAAACAAACCAACCGCTGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTA 1039
Qy 3234 CGCGCAGAAAAAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGTCTGACGCTC 3293
Dy |||||||
Dy 1040 CGCGCAGAAAAAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGTCTGACGC-- 1097
Qy 3294 AGTGAAACGAAACTCAGCTTAAGGGATTTTGGTCAATGACGGATACATATTTGATGTA 3353
Dy |||||||
Dy 1098 ----- 1097
Qy 3354 TTTAGAAAAATAACAAATAGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTGTAT 3413
Dy |||||||
Dy 1098 ----- 1097
Qy 3414 GCGGTGTGAATPACCCACAGATGCGTAAGGAGAAAAATACCGCATCAGGAAATTTGAAGC 3473
Dy |||||||
Dy 1098 ----- 1097
Qy 3474 GTTAATATTCAGAGAACTCGTCAAGAGCGATAGAGCGATGCGGTGGAATCGGG 3533
Dy |||||||
Dy 1098 -----TCAGAGAACTCGTCAAGAGCGATAGAGCGATGCGGTGGAATCGGG 1148
Qy 3534 AGCGCGATACCGTAAAGCAGGAAAGCGGTACGCCATTCGCGCCCAAGCTCTTCAGC 3593
Dy |||||||
Dy 1149 AGCGCGATACCGTAAAGCAGGAAAGCGGTACGCCATTCGCGCCCAAGCTCTTCAGC 1208
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Dy |||||||
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Dy |||||||
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Qy 3834 CATCCGAGTACGTGCTCGATGCGATGTTTTCGCTTGGTGGTTCGAATGGGCGAGTAGC 3893
Dy |||||||
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Qy 3894 CGGATCAAGCGTATGACGCGCGCATTCATCAGCCATGATGATGATCTTTTCGCGCAGG 3953
Dy |||||||
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Qy 4014 TCCCGCTTCAGTGAACAACGCTGAGCAGACAGCTGCGCAAGGAACGCCGCTCGTGGCCAGCCA 4073
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Dy |||||||
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Dy |||||||
Dy 1809 TGTCTGTTGTGCCAGATCATAGCCGAATAGCTCTCCACCCAGCGCGCGGAGAACCTTGC 1868
Qy 4254 GTCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCTCTTCTTGTATCAGACT 4313
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Qy 4314 TGATCCCTCGCCCATCAG 4332
Dy 1929 TGATCCCTCGCCCATCAG 1947
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RESULT 14

AAV40795

ID AAV40795 standard; DNA; 3600 BP.

AC AAV40795;

DT 23-SEP-1998 (first entry)

DE Expected sequence of IGF-I containing plasmid pIG0552.

KW IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;

KW muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;

KW Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.

XX Synthetic.

XX WO9824922-A1.

XX PD 11-JUN-1998.

XX PF 01-DEC-1997; 97WO-US021852.

XX PR 02-DEC-1996; 96US-0031539P.

XX PR 19-NOV-1997; 97US-00974572.

XX (GENE-) GENEMEDICINE INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Coleman M, Schwartz R, Demayo FJ;

XX WPI; 1998-333339/29.

XX New vector for expression of insulin-like growth factor-I - containing a

XX skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'

XX region from growth hormone 3'-UTR.

XX Claim 16; Page 37-41; 115pp; English.

XX This sequence is the expected sequence for pIG0552 which is an example of

XX a vector of the invention. The vector is for expression of a nucleic acid

XX sequence in a cell, and comprises: (a) a nucleic acid cassette containing

XX a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'

XX flanking region including one or more sequences necessary for expression

XX of the nucleic acid cassette, including a promoter from a skeletal alpha-

actin gene; (c) a linker connecting the 5' flanking region to a nucleic acid, the linker having a position for inserting the nucleic acid cassette, and lacking the coding sequence of a gene with which it is naturally associated; and (d) a 3' flanking region, including a 3' untranslated region or a 3' non coding region or both, where the 3' flanking region is 3' to the position for inserting the nucleic acid cassette and comprises a sequence from a growth hormone 3'-UTR. The vector can provide for efficient IGF-I expression, particularly in gene therapy. It can be used for the delivery of IGF-I for treating diseases such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth disorders. They can be used for treating peripheral neuropathies resulting from diabetes, genetic disease such as type I or type II diabetes, genetic disease such as Chacot-marie-tooth disease, ARDS, atherosclerosis, cardiovascular, cerebrovascular, or peripheral vascular disease, haemophilia, inflammation and side-effects from anti-cancer and anti-viral drugs. The vectors can also be used to create transgenic animals for research or livestock improvement

XX Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;

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Qy 2574 TATCCACAGAAATCAGGGGATTAACGAGGAAAGAAATGTGAGCAAAAGGCGCAAAAGG 2633
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Db 800 GACACGACTTATCGCCACTGCGCAGCAGCCACTGTGTAAACAGGATTAGCAGAGCGAGGTATG 859

Qy 3054 TAGCGCGTGTCTACAGAGTCTTGAAGTGTGGCCCTAACTACCGGTCTACACTAGAGGACAG 3113

Db 860 TAGCGCGTGTCTACAGAGTCTTGAAGTGTGGCCCTAACTACCGGTCTACACTAGAGGACAG 919

Qy 3114 TATTGTGTATCTGCGCTCTGCTGAGCCAGTACCTTCGGAAGAGAGTGTGGTACTCTT 3173

Db 920 TATTGTGTATCTGCGCTCTGCTGAGCCAGTACCTTCGGAAGAGAGTGTGGTACTCTT 979

Qy 3174 GATCCGCGCAACCAACCAACCGCTGCTGAGCGGTGGTGTGTTGTTGCAAGCAGCAGATTA 3233

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Qy 3894 CGGATCAAGCGTATGAGCGCGCGCATTTGATCAGCCATGATGATGATGATGATGATGATGATG 3953

Db 1509 CGGATCAAGCGTATGAGCGCGCGCATTTGATCAGCCATGATGATGATGATGATGATGATGATG 1568

Qy 3954 AGCAAGGTGAGATGACAGGAGATCTCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCT 4013

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Qy 4014 TCCGCTTTCAGTGACAGCTGAGCAGCAGCTGGCAGGAAACGCCCTCTGTTGGCAGGCCA 4073

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
12794.750 Million cell updates/sec

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Searched: 41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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11: gb_ges3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	990.6	22.9	1067	1	AU081137 AU081137
4	959.2	22.1	1089	1	AU081124 AU081124
5	898.4	20.7	1049	10	CL021189 CH216-8A1
6	896.6	20.7	1191	8	DR045882 FP-11_A09
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8	871	20.1	951	8	CV983341 UMC-b5f.0
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c	30	789.8	18.2	936	7	CK256977	CK256977	EST740614
c	31	789.8	18.2	947	7	CK298208	CK298208	EST760922
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c	43	781.6	18.0	810	11	DE102302	DE102302	Oryzias 1
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ALIGNMENTS

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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN

DR045845 1186 bp mRNA linear EST 02-JUN-2005
FP-10_F08.SQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.

DR045845
DR045845.1 GI:66909681
EST.
Phaeosphaeria nodorum
Phaeosphaeria nodorum
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Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
1 (bases 1 to 1186)
Blindschneider, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and Oliver, R.P.
cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
Unpublished (2005)
Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.

Location/Qualifiers
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QY 2316 ACATACGAGCCGGAAGCAATAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTCA 2375
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QY 2376 CATTAATGCGTTGCGCTCACTCGCCGCTTTTCAGTCGGGAAACCTGTCGTCGACGTCG 2435
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SOURCE
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  1 (bases 1 to 1176)
AUTHORS
  Xuan,J., Zhao,G., Wang,W., Duan,D., Weng,M. and Wang,B.
TITLE
  Expressed sequence tag analysis of the brown alga Laminaria
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JOURNAL
  Unpublished (2005)
COMMENT
  Contact: Xuan JS
  The State Key Laboratory of Plant Genome Research
  Institute of Genetics and Developmental Biology, Chinese Academy of
  Science
  Datun Road, Chaoyang District, Beijing, China, 100101
  Tel: 086 010 64889353
  Fax: 086 010 64873428
  Email: bnxuan@hotmail.com
  Seq primer: T3 Forward
  High quality sequence stop: 1176.
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     XhoI"
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  Matches 1062; Conservative 0; Mismatches 18;
  Qy      2256  CGTAATCATGTGCTAGCTGTTTCTGTGTGAAATTGTTATCCGCTCAATTCACACA 2315
  Db      37   CGTAATCATGTGCTAGCTGTTTCTGTGTGAAATTGTTATCCGCTCAATTCACACA 96
  Qy      2316  ACATACGAGCGGAGCATAAAGTGTAAAGCTGGGGTGCCTATAGTAGTAACTCA 2375
  Db      97   ACATACGAGCGGAGCATAAAGTGTAAAGCTGGGGTGCCTATAGTAGTAACTCA 156
  Qy      2376  CATTAATTCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTCAGAGTGC 2435
  Db      157  CATTAATTCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTCAGAGTGC 216
  Qy      2436  ATTAATGAATCGGCCAACCGCGGGAGAGCGGTTTCGTAATTGGGCGCTTCCGCTT 2495
  Db      217  ATTAATGAATCGGCCAACCGCGGGAGAGCGGTTTCGTAATTGGGCGCTTCCGCTT 276
  Qy      2496  CCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCACT 2555
  Db      277  CCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCACT 336
  Qy      2556  CAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGAAATGTGAG 2615
  Db      337  CAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGAAATGTGAG 396
  Qy      2616  CAAAGGCGCAGCAAAAGGCGGAGAACCGGTAAAGAGCGCGGTTGCTGGGCTTTTCCATA 2675
  Db      397  CAAAGGCGCAGCAAAAGGCGGAGAACCGGTAAAGAGCGCGGTTGCTGGGCTTTTCCATA 456
  Qy      2676  GGCTCGGCGCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAACC 2735
  Db      457  GGCTCGGCGCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAACC 516
  Qy      2736  CGCAGGACTATAAAGATACACAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCCTG 2795
  Db      517  CGCAGGACTATAAAGATACACAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCCTG 576
  Qy      2796  TTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCG 2855
  Db      577  TTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCG 636
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Qy 2856 TTTCTCAATGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTTCGCTCGCTCAAGCTGG 2915
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Db 637 TTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTTCGCTCGCTCAAGCTGG 696
Qy 2916 GCTGTGTGACGAAACCCCGCTTTCAGCGGAGCCGCTGCGCTTATCCGGTAACTATCGTC 2975
Db 697 GCTGTGTGACGAAACCCCGCTTTCAGCGGAGCCGCTGCGCTTATCCGGTAACTATCGTC 756
Qy 2976 TTGAGTCCAAACCCCGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 3035
Db 757 TTGAGTCCAAACCCCGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 816
Qy 3036 TTACGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGGTGGCTTAACTACG 3095
Db 817 TTACGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGGTGGCTTAACTACG 876
Qy 3096 GCTACACTAGNAGCAGATTTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAA 3155
Db 877 GCTACACTAGNAGCAGATTTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAA 936
Qy 3156 AAAGAGTTGGTAGTCTTTGATCCCGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTG 3215
Db 937 AAAGAGTTGGTAGTCTTTGATCCCGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTG 995
Qy 3216 TTTCCAAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTT 3275
Db 996 TTTCCAAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTT 1053
Qy 3276 CTACGGGGTGTAGCTCAGTGTGAAAGAACTCAGTGTAAAGGATTTTGTCTATGAGCG 3335
Db 1054 CTAC-GGGTCTGACGCTCAGTG---ACGAAACTCAGCTT-AGGGATTTTGTCTATGAGAT 1108
Qy 3336 GATACATA 3343
Db 1109 TATCAAAA 1116

RESULT 3

LOCUS AU081137 1067 bp mRNA linear EST 30-JUL-2002
DEFINITION AU081137 Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone K12, mRNA sequence.
ACCESSION AU081137
VERSION AU081137.1 GI:6431485
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1067)
Kono,T., Sakai,M. and LaPatra,S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
AUTHORS Contact: Masahiro Sakai
TITLE Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
JOURNAL Email: m.sakai@cc.miyazaki-u.ac.jp.
COMMENT Location/Qualifiers
1. 1067
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="K12"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious

hematopoietic necrosis virus"

ORIGIN
Query Match 22.9%; Score 990.6; DB 1; Length 1067;
Best Local Similarity 98.9%; Pred. No. 8.6e-219;
Matches 1018; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
Qy 2210 AGCTCCAGCTTTTGTGTTCCCTTTTGTAGTGAGGTTTAAATTTTCGAGCTTTGGCGTAACTATGTGTC 2259
Db 41 AGCTCCAGCTTTTGTGTTCCCTTTTGTAGTGAGGTTTAAATTTTCGAGCTTTGGCGTAACTATGTGTC 100
Qy 2270 TAGCTGTTTCTGTGTGAAATTTGTATTCGCTCACAATTCACACAACATACGAGCCGGA 2329
Db 101 TAGCTGTTTCTGTGTGAAATTTGTATTCGCTCACAATTCACACAACATACGAGCCGGA 160
Qy 2330 AGCATAAAGTGTAAAGCTGGGTGCTAATAGTGAGTAACTCATTAAATTTGCGTTG 2389
Db 161 AGCATAAAGTGTAAAGCTGGGTGCTAATAGTGAGTAACTCATTAAATTTGCGTTG 220
Qy 2390 CGCTCACTGCCCGCTTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGC 2449
Db 221 CGCTCACTGCCCGCTTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGC 280
Qy 2450 CAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCCGCTTCTCGCTCACTGAC 2509
Db 281 CAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCCGCTTCTCGCTCACTGAC 340
Qy 2510 TCGCTCGCTCGCTCGTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAA 2569
Db 341 TCGCTCGCTCGCTCGTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAA 400
Qy 2570 CGGTTATCCACAGAAATCAGGGGATAACGCAAGGAAAGAACTGTGAGCAAAAGGCGCAGCA 2629
Db 401 CGGTTATCCACAGAAATCAGGGGATAACGCAAGGAAAGAACTGTGAGCAAAAGGCGCAGCA 460
Qy 2630 AAGCCAGGAAACCGTAAAGAGCGGCTTTCGTCGCGGTTTTTCATAGGCTCCGCCCCCT 2689
Db 461 AAGCCAGGAAACCGTAAAGAGCGGCTTTCGTCGCGGTTTTTCATAGGCTCCGCCCCCT 520
Qy 2690 GACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGCAGAGCACTATA 2749
Db 521 GACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGCAGAGCACTATA 580
Qy 2750 AGATACAGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTCGC 2809
Db 581 AGATACAGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTCGC 640
Qy 2810 CTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGGCTTTCTCAATGCTCA 2859
Db 641 CTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGGCTTTCTCATAGCTCA 700
Qy 2870 CGCTGTAGGTATCTCAGTTCGGTGTAGTTCGCTTCAAGCTGGGCTGTGTGCAGCA 2929
Db 701 CGCTGTAGGTATCTCAGTTCGGTGTAGTTCGCTTCAAGCTGGGCTGTGTGCAGCA 760
Qy 2930 CCCCCGCTTCAGCCCGACCGCTGCTTATCCGGTAACTATCTGTAGTCCAAACCG 2989
Db 761 CCCCCGCTTCAGCCCGACCGCTGCTTATCCGGTAACTATCTGTAGTCCAAACCG 820
Qy 2990 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTACGAGCCAGG 3049
Db 821 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTACGAGCCAGG 880
Qy 3050 TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGAGG 3109
Db 881 TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGAGG 940
Qy 3110 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC 3169
Db 941 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC 1000
Qy 3170 TCTTGATCCGGGAAAAACACCCAGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAG 3229

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Db 1001 TCTTGATCCGGAACAAA-CAACGCTGGTAGCGTGTGTTTTTTTTTTGTTGTC-AGCAGCAG 1058
Qy 3230 ATTACGGCG 3238
Db 1059 ATTACGGCG 1067

RESULT 4
AU081124 1089 bp mRNA linear EST 30-JUL-2002
LOCUS AU081124
DEFINITION AU081124 Oncorhynchus mykiss Kidney infected by infectious
henatopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG'12,
mRNA sequence.
ACCESSION AU081124.1 GI:6431472
VERSION AU081124
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1089)
AUTHORS Kono, T., Sakai, M. and LaPatra, S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
1..1089
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="KG'12"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"

FEATURES
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Query Match 22.1%; Score 959.2; DB 1; Length 1089;
Best Local Similarity 97.2%; Pred. No. 1.7e-211;
Matches 1019; Conservative 0; Mismatches 23; Indels 6; Gaps 4;

Qy 2210 AGCTCAGCTTTTGTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGGTCA 2269
Db 42 AGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGGTCA 101
Qy 2270 TAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAATTCACAAACATACAGCCGGA 2329
Db 102 TAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAATTCACAAACATACAGCCGGA 161
Qy 2330 AGCATTAAGTGTAAGACCTTGGGGTGCTTAATGAGTGAGCTAACTCACATTAATTCGGTTG 2389
Db 162 AGCATTAAGTGTAAGACCTTGGGGTGCTTAATGAGTGAGCTAACTCACATTAATTCGGTTG 221
Qy 2390 CGCTCACTCGCGCTTTCAGTCGGGAAACCTGTGTGCGCAGTGATTAATGAATCGGC 2449
Db 222 CGCTCACTCGCGCTTTCAGTCGGGAAACCTGTGTGCGCAGTGATTAATGAATCGGC 281
Qy 2450 CAACGCGCGGAGAGCGGTTTGCGTATTGGCGCTTTCGCTTCCTCGCTCACTGAC 2509
Db 282 CAACGCGCGGAGAGCGGTTTGCGTATTGGCGCTTTCGCTTCCTCGCTCACTGAC 341
Qy 2510 TCGTSCGCTCGGTCGTTTCGCGTTCGCGGCGAGCGGTTATCAGCTCACTCAAAGCGGTAATA 2569
Db 342 TCGTSCGCTCGGTCGTTTCGCGTTCGCGGCGAGCGGTTATCAGCTCACTCAAAGCGGTAATA 401

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Qy 2570 CGGTTATCCACAGATCAGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCAGCAA 2629
Db 402 CGGTTATCCACAGATCAGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCAGCAA 461
Qy 2630 AAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGGTTTTTTTCCATAGGCTCCGCCCCCT 2689
Db 462 AAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGGTTTTTTTCCATAGGCTCCGCCCCCT 521
Qy 2690 GACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 2749
Db 522 GACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 581
Qy 2750 AGATACCAAGCGTTTCCCTCGGAGCTCCCTCGTGGCTCTCTGTTCCACACCTCGCG 2809
Db 582 AGATACCAAGCGTTTCCCTCGGAGCTCCCTCGTGGCTCTCTGTTCCACACCTCGCG 641
Qy 2810 CTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCA 2869
Db 642 CTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCA 701
Qy 2870 CGCTGTAGGTATCTCAGTTCCGTTGAGTCTTCCGTTCCAAAGCTGGGCTGTGTGACGAA 2929
Db 702 CGCTGTAGGTATCTCAGTTCCGTTGAGTCTTCCGTTCCAAAGCTGGGCTGTGTGACGAA 761
Qy 2930 CCCCCGTTTCAGCCGACCGCTCGCCTTATCCGTTAACTATCGTTGAGTCCAAACCG 2989
Db 762 CCCCCGTTTCAGCCGACCGCTCGCCTTATCCGTTAACTATCGTTGAGTCCAAACCG 821
Qy 2990 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTTAGCAGCGAGG 3049
Db 822 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTTAGCAGCGAGG 881
Qy 3050 TATGTAGCGGTGTACAGATTTCTTGAAG-TGGTGGCTTAACACGCTACACGCTACAGTAAG 3108
Db 882 TATGTAGCGGTGTACAGATTTCTTGAAGTTTGTGGCTTAACACGCTACACGCTACAGTAAG 941
Qy 3109 GACAGTATTTGGTATCTCGCTCTCGTGAAGCGAGTTACCTTCGGAAGAGTTGGTAG 3168
Db 942 AACAGTATTTGGTATCTCGCTCTCGTGGAGCCAGTTACCTTCGGAAGAGTTGGTAG 1001
Qy 3169 CTCCTT-GATCCGGCAACAAACCA---CCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGC 3224
Db 1002 CTCCTGGATCCGGCAACAAACCAACCGCTGGGAAGGGGGGTGCTCTTTTGTTCGAAGC 1061
Qy 3225 A-GCAGATTACCGCGAGAAAAAAGGAT 3251
Db 1062 ACGCAGATTACCGCGAGAAAAAAGGAT 1089

RESULT 5
CL021189 1049 bp DNA linear GSS 31-DEC-2003
LOCUS CH216-8A14 RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A14,
DEFINITION genomic survey sequence.
ACCESSION CL021189
VERSION CL021189.1 GI:40463002
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1049)
AUTHORS Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TAGCACTCACTATAGGAGA

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Class: BAC ends		High quality sequence start: 43		High quality sequence stop: 888.	
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Best Local Similarity		98.1%; Pred. No. 2.3e-197;			
Matches 930; Conservative		0; Mismatches 16; Indels 2; Gaps 2;			
QY	2245	TTGAGCTTGGCGTAATCATGTCTAGCTGTTCCTGTGTGAAATTTGTTATCGCTCAC	2304		
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QY	2305	AATTCACACATACGACCGGAAGCATAAAGTGTAAAGCTTGGGCTGCTTAATGAGT	2364		
Db	161	AATTCACACATACGACCGGAAGCATAAAGTGTAAAGCTTGGGCTGCTTAATGAGT	220		
QY	2365	GAGCTAACTCACATTAATTTGGCTTCGCTCACTGCCGCTTTCCAGTCGGGAACCTGTC	2424		
Db	221	GAGCTAACTCACATTAATTTGGCTTCGCTCACTGCCGCTTTCCAGTCGGGAACCTGTC	280		
QY	2425	GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTGGGTATTGGGCG	2484		
Db	281	GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTGGGTATTGGGCG	340		
QY	2485	CTCTTCGGCTTCTCGCTCACTGACTCGCTGGCTCGTTCGCTGGCGGAGCGGT	2544		
Db	341	CTCTTCGGCTTCTCGCTCACTGACTCGCTGGCTCGTTCGCTGGCGGAGCGGT	400		
QY	2545	ATCAGCTCACTCAAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATACGCAGAAA	2604		
Db	401	ATCAGCTCACTCAAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATACGCAGAAA	460		
QY	2605	GAACTGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTCTGC	2664		
Db	461	GAACTGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTCTGC	520		
QY	2665	GTTTTTCATAGCTTCGCGCCCTTGACGAGCATCACAAAATCGAGCTCAAGTCAGAG	2724		
Db	521	GTTTTTCATAGCTTCGCGCCCTTGACGAGCATCACAAAATCGAGCTCAAGTCAGAG	580		
QY	2725	GTGGGGAACCCGACGAGCTATAAAGATACAGCGGTTTCCCTCGTGAAGCTCCCTCGT	2784		
Db	581	GTGGGGAACCCGACGAGCTATAAAGATACAGCGGTTTCCCTCGTGAAGCTCCCTCGT	640		
QY	2785	GGCTCTCTGTTCGACGCTCGCGCTTACCGGATACGTGTCGCTTTTCCCTTCGGG	2844		
Db	641	GGCTCTCTGTTCGACGCTCGCGCTTACCGGATACGTGTCGCTTTTCCCTTCGGG	700		
QY	2845	AAGCGTGGCGCTTCTCAATGCTACGCTGTAGTGTACTCAGTTCGCTGTAGTTCGCTG	2904		
Db	701	AAGCGTGGCGCTTCTCAATGCTACGCTGTAGTGTACTCAGTTCGCTGTAGTTCGCTG	760		
QY	2905	CTCCAAGCTGGGCTGTGTGCAGAACCCCGCTTTCAGCCGACCGCTTCGCTTATCCGG	2964		
Db	761	CTCCAAGCTGGGCTGTGTGCAGAACCCCGCTTTCAGCCGACCGCTTCGCTTATCCGG	820		
QY	2965	TAACTATGCTCTTGAGTCAACCCCGGTAAAGACAGACTTATTCGCACTGGGAGGAGCAC	3024		
Db	821	TAACTATGCTCTTGAGTCAACCCCGGTAAAGACAGACTTATTCGCACTGGGAGGAGCAC	880		

QY	3025	TGTTAAACAGGATTAGCAGACGAGCTATGTAGCGGTTGCTACAGAGTTCTTTGAAGTGGTG	3088		
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QY	3085	GCCTAACTACGGCTACACTAGAGGAC-AGTATTTGGTATCTCGGCTCTCTGAGCCAG	3143		
Db	941	GCCTAACTACGGCTACACTAGAGAACAAAGTATTTGTATCTCGCTCTCTCTGAAACAC	1000		
QY	3144	TTACC-TTCGGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACC	3190		
Db	1001	TTACCTTTTCGAAAAAAGTTGGTAGCTCTTGAATCCGGCAAAAAAAC	1048		
RESULT 6					
LOCUS	DR045882	1191 bp	mRNA	linear	EST 02-JUN-2005
DEFINITION	FP-11_A09_SEQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.				
ACCESSION	DR045882				
VERSION	DR045882.1	GI:66909718			
KEYWORDS	EST.				
SOURCE	Phaeosphaeria nodorum				
ORGANISM	Phaeosphaeria nodorum				
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.				
REFERENCE	1 (bases 1 to 1191)				
AUTHORS	Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and Oliver,R.P.				
TITLE	cDNA library of Phaeosphaeria nodorum grown on wheat cell walls				
JOURNAL	Unpublished (2005)				
COMMENT	Contact: Richard Oliver Australian Centre for Necrotrophic Fungal Pathogens (ACNFP) Murdoch University South Street, Murdoch, W.A 6150, Australia Tel: +0893607404 Email: roliver@murdoch.edu.au.				
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		/db_xref="taxon:13684"			
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ORIGIN					
Query Match 20.7%; Score 896.6; DB 8; Length 1191;					
Best Local Similarity 99.1%; Pred. No. 6e-197;					
Matches 923; Conservative 0; Mismatches 4; Indels 4; Gaps 2;					
QY	2210	AGCTCCAGCTTTGTTCCCTTTAGTAGAGGTTTAATTTTCGAGCTTGGGTTAATCATGTCA	2269		
Db	109	AGCTCCAGCTTTGTTCCCTTTAGTAGAGGTTTAATTTTCGAGCTTGGGTTAATCATGTCA	168		
QY	2270	TAGCTGTTTCCCTGTGCAATTTGTTATCCGCTCACAAATTCACACAACTACGAGCCGA	2329		
Db	169	TAGCTGTTTCCCTGTGCAATTTGTTATCCGCTCACAAATTCACACAACTACGAGCCGA	228		
QY	2330	AGCATAAAGTATA			

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Qy 2570 CGGTTATCCACAGAAATCAGGGGATAAGCCAGGAAGAACATGTGAGCAAAAGGCCAGCAA 2629
Db 469 CGGTTATCCACAGAAATCAGGGGATAAGCCAGGAAGAACATGTGAGCAAAAGGCCAGCAA 528
Qy 2630 AAGGCCAGGAACCGTAAAGAGCCGCGTGTGCGGTTTTCATAGGCTCCGCCCCCT 2689
Db 529 AAGGCCAGGAACCGTAAAGAGCCGCGTGTGCGGTTTTCATAGGCTCCGCCCCCT 588
Qy 2690 GACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 2749
Db 589 GACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 648
Qy 2750 AGATACCAAGGCGTTTCCCGCTTGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCG 2809
Db 649 AGATACCAAGGCGTTTCCCGCTTGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCG 708
Qy 2810 CTTACCGGATACCTGTCCGCTTCTCCCTCGGAGAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCG 2869
Db 709 CTTACCGGATACCTGTCCGCTTCTCCCTCGGAGAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCG 768
Qy 2870 CGCTGTAGTATCTCAGTTCGCTGTAGTCTGCTCCAAAGCTGGGCTGTGTGACGAA 2929
Db 769 CGCTGTAGTATCTCAGTTCGCTGTAGTCTGCTCCAAAGCTGGGCTGTGTGACGAA 828
Qy 2930 CCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCG 2989
Db 829 CCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCG 888
Qy 2990 GTAACACAGCATTAATCCGCTGACGAGCTGCTGAGTCTGCTCCAAAGCTGGGCTGTGTGACGAGG 3049
Db 889 GTAACACAGCATTAATCCGCTGACGAGCTGCTGAGTCTGCTCCAAAGCTGGGCTGTGTGACGAGG 948
Qy 3050 TATGTAGCGGTGTACAGAGTTCCTGAAAGTGGTGGCTTAACTACGCTACACTAGAGG 3109
Db 949 TATGTGCG--CGTGTACAGAGTTCCTGAAAGTGGTGGCTTAACTACGCTACACTAGAG--G 1004
Qy 3110 ACAGTATTGTGATCGCTCTGCTGAAGC 3140
Db 1005 ACAGTATTGTGATCGCTCTGCTGAAGC 1035
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RESULT 7
CB686151/c LOCUS
DEFINITION
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  Bn01b_AAPC_ECORC transgenic Brassica napus overexpressing BNCBF17.c
  onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02008,
  mRNA sequence.
CB686151
CB686151.1 GI:29689876
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 925)
Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.
Expressed Sequence Tags from constitutively frost tolerant
transgenic Brassica napus overexpressing BNCBF17
Unpublished (2002)
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@agr.gc.ca.
Location/Qualifiers
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/organism="Brassica napus"
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Site 2: XhoI; Germinated in soil flats and seedlings grown
for 3 weeks in a Conviron E-15 cabinet set at 20oC/16 hr
light (250 Em-2sec-1) and 16 oC/8 hr dark. Fourth leaves
collected at 9 am and immediately frozen."

ORIGIN
Query Match 20.7%; Score 896.2; DB 6; Length 925;
Best Local Similarity 98.3%; Pred. No. 7.2e-197;
Matches 909; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
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Qy 2820 ACTCTGCGCTCTTCTCCCTTTCGGAAGCGTGGCGCTTCTCAATGCTCACTGCTAGGT 2879
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Qy 2880 ATCTCAGTTCCGTTAGGTTCGTTCCCTCAAGCTGGCTGTGTGACGAAACCCCGGTTTC 2939
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Db 146
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Qy 3120 GTATCTGGCTCTGCTGAAGCCAGT 3144

Db 25 GTATCTGGCTCTGCTGAAGCCAGT 1

RESULT 8

CV983341

LOCUS UMC-bof OA01-002-g06.Ovarian Follicle bof Bos taurus CDNA 3', mRNA

DEFINITION CV983341 951 bp linear EST 30-NOV-2004

ACCESSION CV983341

VERSION CV983341.1

KEYWORDS GI:56144062

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

AUTHORS Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C., Roberts, R.M., Smith, M.F. and Youngquist, R.S.

TITLE USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female Reproduction

JOURNAL Unpublished (2002)

COMMENT Contact: DNA Core Facility (Bovine Project) Animal Science - RS Prather University of Missouri-Columbia M616 Medical Sciences Bldg., Columbia, MO 65212, USA Tel: (573) 882-0428 Fax: (573) 884-5552 Email: bovine@net.missouri.edu POLYA=No.

FEATURES

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Location/Qualifiers

1..951

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/dev_stage="Ovarian Follicle"

/clone_lib="bof"

/note="Vector: pSPORT1; Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather (Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.mst.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification

with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at 37 degrees with 10mcg of NotI-tag-dt18 oligonucleotide (GCTGCTCGCGCGC-tag-T18) and reverse transcribed at 37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dt18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core Facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res. 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didiion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(A) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A Efstratiadis, 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG_TISSUE=Ovarian Follicle

[illegible][illegible]

Db CTATAAGATACACAGGCTTTCCCTCCCTGGAAGCTCCCTGCTGCTCTCTCTGCGACC 420
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Db GCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGTGGCGCTTACAGGCTACA 720
QY CTAGAAGACA-GTATTGTGTATCT-GCGCTCTGCTGAAGCC---AGTTACCTTCGAAA 3156
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RESULT 10
LOCUS CL076016
DEFINITION CH216-138F20, RM1.1 CH216 Xenopus tropicalis genomic clone
ACCESSION CH216-138F20, genomic survey sequence.
VERSION CL076016
KEYWORDS CL076016.1 GI:40531929
SOURCE GSS.

ORGANISM Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 885)
AUTHORS Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E., and Wilson, R.

TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TAGCACTACTATAGGAGA
Class: BAC ends
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Location/Qualifiers
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BAC library"

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QY 2528 CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTATACGTTATCCACAGATCA 2587
Db 245 CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTATACGTTATCCACAGATCA 304
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Db 305 GGGGATAACGCGAGGAAAGCAATGTGAGCAAAAGGCGCAGCAAAAGGCGAGGAA 364
QY 2648 AAGGCGCGTGTGCTGCGGCTTTTTCATAGGCTCGGCGCTGCTGAGGAGCATCAAA 2707
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QY 2708 CGACGCTCAAGTCAGAGGTGGGAAACCGGACAGGACTATAAAGATACAGGCGTTC 2767
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Db 725 CCACTGGCAGCAGCCTATGTTAAGATTAAGAGCGAGGTATCTAGCGGTGCTTACA 784
QY 3068 GAGTCTTCTGAAGTGTGGCTTAAGTACGCTACCTAGAGGAGCAGTATTTGTTGTC 3127
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DR046031 1195 bp mRNA linear EST 02-JUN-2005

FP-8 F02_SEQ cDNA library of Phaeosphaeria nodorum grown on wheat

cell_walls Phaeosphaeria nodorum cDNA, mRNA sequence.

ACCESSION DR046031

VERSION DR046031.1 GI:66909867

KEYWORDS EST.

SOURCE Phaeosphaeria nodorum

ORGANISM Phaeosphaeria nodorum

Phaeosphaeria nodorum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;

Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.

1 (bases 1 to 1195)

Bindshedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and

Oliver,R.P.

cDNA library of Phaeosphaeria nodorum grown on Wheat cell walls

Unpublished (2005)

Contact: Richard Oliver

Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)

Murdoch University

South Street, Murdoch, W.A 6150, Australia

Tel: +0893607404

Email: roliver@murdoch.edu.au.

Location/Qualifiers

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Best Local Similarity 97.2%; Pred. No. 5.9e-187;

Matches 902; Conservative 0; Mismatches 19; Indels 7; Gaps 3;

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QY 2270 TAGCTGTTTTCGTGTGAATTTGTTATCCGCTCACAAATCCACAAATACAGCCGGA 2329

Db 224 TAGCTGTTTTCGTGTGAATTTGTTATCCGCTCACAAATCCACAAATACAGCCGGA 283

QY 2330 AGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGTAACTACATTAATTGGTTG 2389

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QY 2390 CGCTACTCGCCGCTTCAGTCGGGAACCTGTCGCGAGCTGATTAATGAATCGGC 2449

Db 344 CGCTCACTCGCCGCTTCAGTCGGGAACCTGTCGCGAGCTGATTAATGAATCGGC 403

QY 2450 CAAACGCGGGGAGAGCGGTTTGCCTATTGGCGCTCTTCGCGCTTCCTCGCTCACTGAC 2509

Db 404 CAAACGCGGGGAGAGCGGTTTGCCTATTGGCGCTCTTCGCGCTTCCTCGCTCACTGAC 463

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QY 2570 CGGTTATCCACAATCCGGGTAACCGAGGAAGAAACATGTGACAAAGCCAGCAA 2629

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RESULT 12

LOCUS CX012952

DEFINITION ioc62d12.bi Whole Heart Library (DOGEST5) Canis familiaris cDNA,

mRNA sequence.

ACCESSION CX012952

VERSION CX012952.1 GI:56395363

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

Canis.

1 (bases 1 to 875)

Baliya,V.S., Nascimento,L.U. and McCombie,W.R.

ESTs from Canis familiaris whole heart (dog)

Unpublished (2004)

Contact: W. Richard McCombie

Lita Auenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Location/Qualifiers

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/note="Organ: Heart; Vector: pBluescript II SK; Site:1:

XR kit from Stratagene. Cloned cDNA was size selected

between 1-3 kb. Mark Haskins VMD, PhD, pathology and

Medical Genetics, School of Veterinary Medicine,

University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

FEATURES

source

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XR kit from Stratagene. Cloned cDNA was size selected

between 1-3 kb. Mark Haskins VMD, PhD, pathology and

Medical Genetics, School of Veterinary Medicine,

University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

ORIGIN

Query Match 19.7%; Score 852; DB 8; Length 875;
Best Local Similarity 98.8%; Pred. No. 1.3e-186;
Matches 858; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 2555 TCAAGGCGGTAATACGCTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTGA 2614
DB 128 TCAAGGCGGTAATACGCTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTGA 187

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QY 2675 AGGCTCCGCCCCCTGACGACATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAAC 2734
DB 248 AGGCTCCGCCCCCTGACGACATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAAC 307

QY 2735 CCGACAGGACTATAAGATACGAGCGCTTCCCTCGAAGCTCCCTCGTGGCTCTCCT 2794
DB 308 CCGACAGGACTATAAGATACGAGCGCTTCCCTCGAAGCTCCCTCGTGGCTCTCCT 367

QY 2795 GTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTGGCG 2854
DB 368 GTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTGGCG 427

QY 2855 CTTTCTCAATGCTACGCTGAGTACTCAGTTTCGCTGAGTTCGCTTCCCAAGCTG 2914
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AU081044
LOCUS 1163 bp mRNA linear EST 30-JUL-2002
DEFINITION AU081044 Oncorhynchus mykiss Kidney infected by infectious
hematopoietic necrosis virus
mRNA sequence.
ACCESSION AU081044

AU081044.1 GI:6431392
EST
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1163)
Kono T., Sakai M. and Lapetra S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 mishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
1. 1163
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/clone_lib="Oncorhynchus mykiss Kidney infected by
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/notes="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"
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Matches 835; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 2270 TAGCTGTTTCTGCTGTAATTTGTTATTCGCTCACAATTCACACATCAGAGCCGGA 2329
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DB 446 AGCATTAAGTAAAGCTGGGCTGCTTATGAGTGAAGTAACTCAATTAATTCGCTG 505

QY 2390 CGTCACTGCGCTTTTCCAGTCGGGAAACCTGCTGCGCAGCTGCAATTAATGAATCGGC 2449
DB 506 CGTCACTGCGCTTTTCCAGTCGGGAAACCTGCTGCGCAGCTGCAATTAATGAATCGGC 565

QY 2450 CAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTTTCGCTTCTCGCTCACTGAC 2509
DB 566 CAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTTTCGCTTCTCGCTCACTGAC 625

QY 2510 TCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2569
DB 626 TCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 685

QY 2570 CGGTTATCCACAGATCAGGGGATACGCAAGGAAAGCAATGTGAGCAAAAGGCGCAGCA 2629
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Db 926 CTTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCA 985

Qy 2870 CGCTGTAGGTATCTCAGTTCGGTGTAGGTGTCGCTCCAAAGCTGGGCTGTGTGCAGAA 2929

Db 986 CGCTGTAGGTATCTCAGTTCGGTGTAGGTGTCGCTCCAAAGCTGGGCTGTGTGCAGAA 1045

Qy 2930 CCCCCGTTTACGCGGACCGTGGCGCTTATCCGGTAACTATGCTTCGTGATCTCAACCCG 2989

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Db 1105 GTAAGACACGACTTATCCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAG 1163

RESULT 14
CV984340

LOCUS CV984340 868 bp mRNA linear EST 30-NOV-2004

DEFINITION UMC-bov 0A02-010-e02 Oviduct bov Bos taurus CDNA 3', mRNA sequence.

ACCESSION CV984340

VERSION CV984340.1 GI:56145061

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 868)

Prather, R.S., Smith, M.F. and Youngquist, R.S.

Roberts, R.M., Smith, M.F. and Youngquist, R.S.

USDA Grant NRI-2002-03476; Bovine ESTs: Focus on Female Reproduction

Unpublished (2002)

Contact: DNA Core Facility (Bovine Project)

Animal Science - RS Prather

University of Missouri-Columbia

M616 Medical Sciences Bldg., Columbia, MO 65212, USA

Tel: (573)882-0428

Fax: (573)884-5552

Email: bovine@net.missouri.edu

POLYA=No.

FEATURES

Source

1..868

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/db_xref="taxon:9913"

/clone_lib="bov"

/note="Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather, E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: Germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.net.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures

have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the SuperScript plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at 637 degrees with 10mcg of NotI-tag-drl8 oligonucleotide (GCTGCTGGCGCGC-tag-118) and reverse transcribed at 437 degrees with Superscript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-drl8 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's Bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JB, Whitworth KM, Green JA, Forrester LJ, Springer GK, Dildion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing

CDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bernaldo, P Jelene, L Su, L Lawton, A Efsiratidis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.

ORIGIN

Query Match	19.0%;	Score 821.2;	DB 8;	Length 868;
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RESULT 15
AG332951

AG332951 . 1169 bp DNA linear GSS 18-DEC-2004
Mus musculus molossinus DNA, clone:MSMg01-123F02.T7, genomic survey
sequence.

Accession
Version

KEYWORDS
SOURCE
GSS.
Mus musculus molossinus (Japanese wild mouse)

ORGANISM
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS

ABE, K., KOGANE, M., IZUGAWA, K., IZUMIYAMA, M., ITOYODA, A., KOJIMA, I.,
EZAWA, K., SAITOU, N., HATTORI, M., SAKAKI, Y., MORIWAKI, K. and
SHIROISHI, T.

TITLE Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis

JOURNAL Genome Res. 14 (12): 2439-2447 (2004)

BOOKMATE
PUBMED
15574823
2 (bases 1 to 1169)
GENOME REF: 14 (12); 2439-2447 (2004)
REFERENCE

REFERENCE	AUTHORS	TITLE
2 (Pages 1 to 1165)	Hattori, M., Toyoda, A	Direct Submission

JOURNAL
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: <http://hgp.gsc.riken.go.jp/>,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSWg01. For BAC library availability, please contact Kuniya Abe (abe@rc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rc.riken.jp

PRIMERS
Sequencing : T7

LIBRARY
Vector : pBACe3.6

R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES	Location/Qualifiers
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5	1586.2	36.6	4644	3	US-09-481-355-19
6	1586.2	36.6	4644	3	US-09-481-282-19
7	1586.2	36.6	4644	3	US-09-455-659A-19
8	1586.2	36.6	4644	3	US-09-484-995-19
9	1586.2	36.6	4644	3	US-09-479-123-19
10	1586.2	36.6	4644	3	US-09-484-317A-19
11	1586.2	36.6	4644	3	US-09-276-820A-19
12	1586.2	36.6	5247	3	US-09-479-123-20
13	1586.2	36.6	5247	3	US-09-484-997-20
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 QY 3360 -----AAAATAACAAATAGGGTTCCGCGCACATTTCCCGCAAAAG 3401
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 QY 7169 TGGTCGGTCAATTCGAAACCCCAAGTCCGCTCAGAAAGAACTCGTCAAGAGCGGATAGA 7228
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 QY 7349 CGGCCACACCCAGCGCCACAGTCCGATGAATCAGAAAAAGCGCCATTTTCCACCATGA 7408
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 QY 7889 CGCGCGCATCAGACGCGGATTTGCTGTTGCGCCAGTCATAGCCGAATAGCCTCTCCA 7948
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 QY 4232 CCCAAGCGCGGAGAACCTCGTGCAATCATCTTGTTCATATGTCGAAACGATCTCTC 4291
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 QY 7949 CCCAAGCGCGGAGAACCTCGTGCAATCATCTTGTTCATATGTCGAAACGATCTCTC 8008
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 QY 4292 ATCTGCTCTTGTATCAGAGCTTGTATCCCTGCGCCATCAG 4332
 DB |||||
 QY 8009 ATCTGCTCTTGTATCAGATCTTGTATCCCTGCGCCATCAG 8049
 DB |||||

RESULT 2
 US-08-472-809B-8
 ; Sequence 8, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/472.809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-8

Query Match 39.7%; Score 1719; DB 2; Length 5707;
Best Local Similarity 90.8%; Pred. No. 1.2e-280;
Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;
Qy 2214 CCAGCTTTTGTTCCTTTAGTGGGTTAAATTCGAGCTTGGCGTAAATCATGTGTCATAGC 2273
Db 3477 CCAGCTTTTGTTCCTTTAGTGGGTTAAATTCGAGCTTGGCGTAAATCATGTGTCATAGC 3536
Qy 2274 TGTTCCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAACATACGAGCGGAGCA 2333
Db 3537 TGTTCCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAACATACGAGCGGAGCA 3596
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Db 3597 TAAAGTGAAGCCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTGCGCT 3656
Qy 2394 CACTGCCCGCTTTCCAGTCGGGAAACCTGTGCTGCGAGCTGCATTAATGAATCGGCCAAC 2453
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Qy 2454 GCGCGGGAGAGCGGTTTCGCTATTGGCGCTCTTCGCTTCTCGCTCACTGACTCGC 2513
Db 3717 GCGCGGGAGAGCGGTTTCGCTATTGGCGCTCTTCGCTTCTCGCTCACTGACTCGC 3776
Qy 2514 TGGCTCGGTCGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGT 2573
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Db 4017 ACCAGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCGCTTA 4076
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Db 4077 CCGGATACCTGTCGGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCAATGCTCAGCT 4136
Qy 2874 GTAGGTATCTCAGTTTCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCACGAAACCC 2933
Db 4137 GTAGGTATCTCAGTTTCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCACGAAACCC 4196
Qy 2934 CCGTTACGCGCGAGCGCTGGCGCTTATTCGGTAACTATTCGTTGAGTCAACCCGGTAA 2993
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Qy 2994 GACACGACTTATCGCACTGGCAGCAGCACTGTAACAGATTTAGCAGAGCGAGGTATG 3053
Db 4257 GACACGACTTATCGCACTGGCAGCAGCACTGTAACAGATTTAGCAGAGCGAGGTATG 4316
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Db 4437 GATCCGCAAAACAAACACCGCTGTGAGCGTGTGTTTGTGTTGCAACGACAGATTA 4496
Qy 3234 CCGCGAGAAAAAAGGATCTCAAGAAAGATCTTTTGTGATCTTTTCTACGGGTCTGACGCTC 3293
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Db 4606 AGCGCGATACCGTAAAGCACAGAGAGCGGTGAGCGCATTTCCGCGCAAGCTCTTCAGC 4665
Qy 3594 AATATCAGCGGTAGCAACGCTATGTCTGATAGCGGTGCGCACACCCAGCGCGCAC 3653
Db 4666 AATATCAGCGGTAGCAACGCTATGTCTGATAGCGGTGCGCACACCCAGCGCGCAC 4725
Qy 3654 GTGATGAATTCAGAAAAAGCGCATTTTCCACCATGATATTCGGCAGCAGGATCGCC 3713
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Qy 3834 CATCCGAGTACGCTCGCTCGATGCTGTTTTCGCTTGTGTCGATCGGCGAGGTAGC 3893
Db 4906 CATCCGAGTACGCTCGCTCGATGCTGTTTTCGCTTGTGTCGATCGGCGAGGTAGC 4965


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2456 TCATCTGTATGCAAGACCGGCTTCATCCGAGTAGTCTGCTCGATGCGATGTTTC 2515
3868 GCTTGTGTGTCGAATGGGAGGAGTAGCCGATCAAGCGTATGACGCGCCGATGTCATCA 3927
2516 GCTTGTGTGTCGAATGGGAGGAGTAGCCGATCAAGCGTATGACGCGCCGATGTCATCA 2575
3928 GCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTCCCGGCG 3987
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RESULT 4

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US-09-484-997-19
; Sequence 19, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-997-19

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Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
 Best Local Similarity 96.0%; Pred. No. 2.8e-258;

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Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
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QY 3748 CTGCGCTTGAGCCTGGCGAAGCAGTTGGGTGGCGCGAGCCCTGTATGCTCTTGTGTCAGA 3807
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QY 2396 CTGCGCTTGAGCCTGGCGAAGCAGTTGGGTGGCGCGAGCCCTGTATGCTCTTGTGTCAGA 2455
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QY 3808 TCATCTGATGTCAGCAAGCAGGCTTCCATCGAGTACGTGCTCGCTCGATGCGATGTTTC 3867
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QY 2456 TCATCTGATGTCAGCAAGCAGGCTTCCATCGAGTACGTGCTCGCTCGATGCGATGTTTC 2515
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QY 2636 ACTTCGCCCAATAGCAGCAGTCCCTTCCGCTTTCAGTGACAAAGTGCAGCACAGCTGCG 2695
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QY 2756 AGGGACCGGACAGTCTGCTTTCAGCAAAAGAACCGGCGCCCTGCGCTGACAGCGG 2815
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QY 2816 AACAGCGCGCATCAGACAGCGCATCTGCTGTTGTCGCCAGTCAATGCCAATAGCCTC 2875
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QY 4228 TCCACCCAGCGCGCGAGAACCTCGCTGTCGAATCCATCTGTTCAATCATCGAAACGAT 4287
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QY 2876 TCCACCCAGCGCGCGAGAACCTCGCTGTCGAATCCATCTGTTCAATCATCGAAACGAT 2935
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RESULT 5

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US-09-481-355-19
; Sequence 19, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-355-19
Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
QY 2608 CATGTGAGCAAAAGGCCAGCAAAAGCCAGAAACCGTTAAAGAGCCCGCTTGTGTCGGTT 2667
Db |||||
QY 1302 CATGTGAGCAAAAGGCCAGCAAAAGCCAGAAACCGTTAAAGAGCCCGCTTGTGTCGGTT 1361
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QY 2668 TTTCCATAGGCTCGCCCCCTGACGAGCATCAAAAGATCGAGCTCCCTCGTGGC 2727
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RESULT 6
US-09-481-282-19
; Sequence 19, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-282-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

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RESULT 7
US-09-455-659A-19
; Sequence 19, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-455-659A-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
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RESULT 8

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US-09-484-996-19
; Sequence 19, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; ENDGENOUS GENES
; FILE REFERENCE: 0221-0003H

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; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-484-996-19

Query Match      36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

QY 2608 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCGCGGTTGCTGGCGTT 2667
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RESULT 9

US-09-479-123-19

; Sequence 19, Application US/09479123

; Patent No. 6670185

; GENERAL INFORMATION:

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; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-479-123-19
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Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

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RESULT 10

US-09-484-317A-19
; Sequence 19, Application US/09484317A
; Patent No. 6740503
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: ATX-007CP4DV11
; CURRENT APPLICATION NUMBER: US/09/484,317A
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-317A-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
QY 2608 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGCCCGTTGCTGGCGTT 2667
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RESULT 11
 US-09-276-820A-19
 ; Sequence 19, Application US/09276820A
 ; Patent No. 6897066
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; FILE REFERENCE: 0221-0003US
 ; CURRENT APPLICATION NUMBER: US/09/276,820A
 ; CURRENT FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 4644
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-276-820A-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
 Best Local Similarity 96.0%; Pred. No. 2.8e-258;
 Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

Qy 2608 CATGTGACAAAAGCGCCAGCAAAAAGCGCAGAAACCGTAAAAAGCGCGGTTCGTGGCGTT 2667
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RESULT 12
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 ; Sequence 20, Application US/09479122
 ; Patent No. 6410266
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERF, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; FILE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003C
 ; CURRENT APPLICATION NUMBER: US/09/479,122
 ; CURRENT FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: 09/276,820
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 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 5247
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-479-122-20

Query Match 36.6%; Score 1586.2; DB 3; Length 5247;
 Best Local Similarity 96.0%; Pred. No. 2.8e-258;
 Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

QY 2608 CATGTGAGCAAAAGGCGCAGGAGAACCGTAAAGGCGCGCTTGTGGCGTT 2667
 Db 1250 CATGTGAGCAAAAGGCGCAGGAGAACCGTAAAGGCGCGCTTGTGGCGTT 1309
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 Db 1310 TTTTCATAGGCTCCGCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTG 1369
 QY 2728 GCGAAACCGCAGCAGGACTATAAGATACAGGGGTTTCCCTCGGAAGCTCCCTCGTGG 2787
 Db 1370 GCGAAACCGCAGCAGGACTATAAGATACAGGGGTTTCCCTCGGAAGCTCCCTCGTGG 1429
 QY 2788 CTCTCTGTTCGACCGCTTACCGGATACCGGCTTCTCCCTTCGCGGAAG 2847
 Db 1430 CTCTCTGTTCGACCGCTTACCGGATACCGGCTTCTCCCTTCGCGGAAG 1489
 QY 2848 CGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTGGGTAGGTCTGTCGCTC 2907
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 QY 2908 CAACTGGGCTGTGTGACGAAACCCCGCTTACGCGCGACCGCTGGCGCTTATCCGGTAA 2967
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RESULT 13
US-09-484-997-20
; Sequence 20, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-484-997-20
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Db 1250 CATGTAGCAAAAGGCGCAGAAAGGCGCAGAAACCGTAAAAAGGCGCGTTCGTCGCGTT 1309
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RESULT 14
 US-09-481-355-20
 ; Sequence 20, Application US/09481355
 ; Patent No. 6524824
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; FILE REFERENCE: 0221-0003F
 ; CURRENT APPLICATION NUMBER: US/09/481,355
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
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 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 5247
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-481-355-20

Query Match 36.8%; Score 1586.2; DB 3; Length 5247;
 Best Local Similarity 96.0%; Pred. No. 2.8e-258;
 Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
 Qy 2608 CATGTGAGCAAAAGGCGCAGCAAAAGCGCAGAACCGTAAAGAGCGCGCTTGTGGCGTT 2667
 Db 1250 CATGTGAGCAAAAGGCGCAGCAAAAGCGCAGAACCGTAAAGAGCGCGCTTGTGGCGTT 1309
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 Qy 2788 CTCTCTGTTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAG 2847
 Db 1430 CTCTCTGTTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAG 1489
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RESULT 15
US-09-481-282-20
; Sequence 20, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
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Job time : 1306 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 20:09:48 ; Search time 2964 Seconds
(without alignments)

12086.014 Million cell updates/sec

Title: US-10-811-028A-1

Perfect score: 4331

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4170.6	96.3	4293	8	US-10-811-028A-2
3	3245.6	74.9	4187	8	US-10-811-028A-6
4	3147.8	72.7	4058	8	US-10-811-028A-5
5	2341.8	54.1	5753	8	US-10-811-028A-3
6	2341.8	54.1	5760	8	US-10-811-028A-4
7	1937	44.7	3609	5	US-10-234-406-3
8	1924.4	44.4	3589	5	US-10-234-406-1
9	1923.8	44.4	3589	6	US-10-136-837-4
10	1845.4	42.6	8249	6	US-10-136-837-2
11	1845.4	42.6	11546	6	US-10-136-837-1
12	1719	39.7	3600	3	US-09-861-101-2
13	1718.4	39.7	2192	5	US-10-021-403A-10
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ALIGNMENTS

RESULT 1

US-10-811-028A-1
Sequence 1, Application US/10811028A
Publication No. US20050043258A1

GENERAL INFORMATION:

APPLICANT: Bennett, Michael

APPLICANT: Chen, Yen-Ju

APPLICANT: Genteric, Inc.

TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia

FILE REFERENCE: 020714-002410US

CURRENT APPLICATION NUMBER: US/10/811.028A

CURRENT FILING DATE: 2004-03-25

PRIOR APPLICATION NUMBER: US 60/458,793

PRIOR FILING DATE: 2003-03-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 4332

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:pMB1-MnSOD

OTHER INFORMATION: plasmid expression vector

FEATURE:

NAME/KEY: modified_base

LOCATION: (1979)

OTHER INFORMATION: n = g, a, c or t

US-10-811-028A-1

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				Indels	0;
				Gaps	0;
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Qy	61	TAAGTTGGGTAACGCCAGGGTTTCCAGTCACGACGTTGTAACACGACGCGCCAGTGAAT	120		
Db	61	TAAGTTGGGTAACGCCAGGGTTTCCAGTCACGACGTTGTAACACGACGCGCCAGTGAAT	120		
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 : Publication No. US20050043258A1
 : GENERAL INFORMATION:
 : APPLICANT: Bennett, Michael
 : APPLICANT: Chen, Yen-Ju
 : APPLICANT: Genteric, Inc.
 : TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
 : FILE REFERENCE: 020714-002410US
 : CURRENT APPLICATION NUMBER: US/10/811,028A
 : CURRENT FILING DATE: 2004-03-25

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; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-HAMnSOD
; OTHER INFORMATION: plasmid expression vector
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1940)
; OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-2

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Best Local Similarity 98.2%; Pred. No. 0;
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Db      481  CATCAAGTGTATCATATGCAAGTACGCCCTTATTTGACGTCAATGACGTAAATGGCCC 540

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RESULT 3
 US-10-811-028A-6
 ; Sequence 6, Application US/10811028A
 ; Publication No. US20050043258A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Michael
 ; APPLICANT: Chen, Yen-Ju
 ; APPLICANT: Genteric, Inc.
 ; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
 ; FILE REFERENCE: 020714-002410US
 ; CURRENT APPLICATION NUMBER: US/10/811,028A
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: US 60/458,793
 ; PRIOR FILING DATE: 2003-03-26
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 4187
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:pMB1-EcSOD
 ; OTHER INFORMATION: plasmid expression vector
 US-10-811-028A-6

Query Match 74.9%; Score 3245.6; DB 8; Length 4187;
 Best Local Similarity 86.2%; Pred. No. 0;
 Matches 3733; Conservative 0; Mismatches 454; Indels 145; Gaps 7;

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Qy 4081 CGCGTGCCTCGTCTTTCGAGTTCATTCAGGGCAGCGGACAGGTGGTCTTGACAAAAAGA 4140
Db 3936 CGCGTGCCTCGTCTTTCGAGTTCATTCAGGGCAGCGGACAGGTGGTCTTGACAAAAAGA 3995
Qy 4141 ACCGGGCGCCCTGCGCTGACGCGGAGACAGCGGCGCATCAGACGCGCATTTGCTGT 4200
Db 3996 ACCGGGCGCCCTGCGCTGACGCGGAGACAGCGGCGCATCAGACGCGCATTTGCTGT 4055
Qy 4201 TGTGCCAGTATAGCCGAATAGCTCTTCCACCCAGCGCGGAGAACCTGCGTGCAT 4260
Db 4056 TGTGCCAGTATAGCCGAATAGCTCTTCCACCCAGCGCGGAGAACCTGCGTGCAT 4115
Qy 4261 CCATCTTGTTCATCATCGGAACGATCTCATCTCTCTCTTGTATCAGAGCTTGATCCC 4320
Db 4116 CCATCTTGTTCATCATCGGAACGATCTCATCTCTCTCTTGTATCAGAGCTTGATCCC 4175
Qy 4321 CTGCGCCATCAG 4332
Db 4176 CTGCGCCATCAG 4187

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RESULT 4
US-10-811-028A-5
; Sequence 5, Application US/10811028A
; Publication NO. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Genteric, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: pMB1-hIFN-alpha
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-5

Query Match 72.7%; Score 3147.8; DB 8; Length 4058;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 3710; Conservative 0; Mismatches 348; Indels 274; Gaps 8;

Qy 1 CGGTGCGGGCTCTTCGCTATTTAGCCAGCTGGCGAAGGGGGATGTGCTCAAGCGAT 60
Db 1 CGGTGCGGGCTCTTCGCTATTTAGCCAGCTGGCGAAGGGGGATGTGCTCAAGCGAT 60
Qy 61 TAAGTTGGGTAAACGCCAGGGTTTCCAGTCACGACCTTGTAAACGACGCCAGTGAAT 120
Db 61 TAAGTTGGGTAAACGCCAGGGTTTCCAGTCACGACCTTGTAAACGACGCCAGTGAAT 120
Qy 121 TGTAAATACGACTCACTATAGGGCGAATTTGGGTACTGGCCACAGAGCTTGGCCCATTTGAT 180
Db 121 TGTAAATACGACTCACTATAGGGCGAATTTGGGTACTGGCCACAGAGCTTGGCCCATTTGAT 180
Qy 181 ACGTGTATCCATATCAATATATGTAATTTATTTATTTGGCTCATGTCCAAATTAACGCCA 240
Db 181 ACGTGTATCCATATCAATATATGTAATTTATTTATTTGGCTCATGTCCAAATTAACGCCA 240
Qy 241 TGTTCACATTTGATTTAGCTAGTTTAAATAGTAATCAATTTACGGGTCTATTAGTTTCA 300
Db 241 TGTTCACATTTGATTTAGCTAGTTTAAATAGTAATCAATTTACGGGTCTATTAGTTTCA 300
Qy 301 AGCCCATATATGAGTTCCGCTTTACATACTTACGGTAAATGGCCCGCTGGCTGACCG 360
Db 301 AGCCCATATATGAGTTCCGCTTTACATACTTACGGTAAATGGCCCGCTGGCTGACCG 360
Qy 361 CCCAACGACCCCGCCCATTTGACATTAATAGTATGTTTCCATAGTAACGCCAATA 420
Db 361 CCCAACGACCCCGCCCATTTGACATTAATAGTATGTTTCCATAGTAACGCCAATA 420
Qy 421 GGGACTTTCATTTGACGTCATGTTGGTGGAGTATTTAGGTAACTTGGCCACTTGGCAGTA 480
Db 421 GGGACTTTCATTTGACGTCATGTTGGTGGAGTATTTAGGTAACTTGGCCACTTGGCAGTA 480
Qy 481 CATCAAGTGTATCATATGCCAAGTACGCCCTTATTTGACGTCATTAATGGCGTAAATGGCCC 540
Db 481 CATCAAGTGTATCATATGCCAAGTACGCCCTTATTTGACGTCATTAATGGCGTAAATGGCCC 540
Qy 541 GCCTGGCATTAATGCCAGTACATGACCTTATGGGACTTTTCTTCTTGGCAGTACATCTAC 600
Db 541 GCCTGGCATTAATGCCAGTACATGACCTTATGGGACTTTTCTTCTTGGCAGTACATCTAC 600
Qy 601 GTATTAGTCATCGCTTATTTACCATGTTGATGCGGTTTGGCAGTACATCAATGGGCGTGA 660
Db 601 GTATTAGTCATCGCTTATTTACCATGTTGATGCGGTTTGGCAGTACATCAATGGGCGTGA 660
Qy 661 TAGCGTTTGTACTCAAGGAGTTTCCAAAGTCTCCACCCCATTTGACGTCATTAATGGGAGTTG 720
Db 661 TAGCGTTTGTACTCAAGGAGTTTCCAAAGTCTCCACCCCATTTGACGTCATTAATGGGAGTTG 720
Qy 721 TTTTGGCACCAAAATCAAGGAGCTTTTCCAAATGTCGTAACACTCGCCCGCATTTGAG 780
Db 721 TTTTGGCACCAAAATCAAGGAGCTTTTCCAAATGTCGTAACACTCGCCCGCATTTGAG 780
Qy 781 CAAATGGGCGGTAGCGGTGATCGGTGGAGGTCATATATAGCAGAGCTCGTTTAGTGAAC 840
Db 781 CAAATGGGCGGTAGCGGTGATCGGTGGAGGTCATATATAGCAGAGCTCGTTTAGTGAAC 840
Qy 841 CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTGTACCTTCCATAGAGACACCGGGAC 900
Db 841 CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTGTACCTTCCATAGAGACACCGGGAC 900
Qy 901 CGATCCAGCTGACTCTAGCTAGCTTGAAGTTCGTGAGGCGCTCGGGCAGGTTGTTGT 960
Db 901 CGATCCAGCTGACTCTAGCTAGCTTGAAGTTCGTGAGGCGCTCGGGCAGGTTGTTGT 960
Qy 961 ATCAAGGTTTACAAAGACAGGTTTAAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGA 1020

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Qy 3181 CAAACAAACACCGCTGCTAGCGTGGTGTGTTTTTTTGGTTGCAAGCAGCAGATTACGCCGAG 3240
Db 2907 CAAACAAACACCGCTGCTAGCGTGGTGTGTTTTTTTGGTTGCAAGCAGCAGATTACGCCGAG 2966
Qy 3241 AAAAAAGGATCTCAAGAAGTCTTTTGTGATCTTTTCTACGGGCTCAGCGTCAAGTGAA 3300
Db 2967 AAAAAAGGATCTCAAGAAGTCTTTTGTGATCTTTTCTACGGGCTCAGCGTCAAGTGAA 3026
Qy 3301 CGAAATCTCAGCTTAAGGATTTTGGTTCATGAGCGGATACATATTGAAATGATTTAGAA 3360
Db 3027 CGAAATCTCAGCTTAAGGATTTTGGTTCATGAGCGGATACATATTGAAATGATTTAGAA 3086
Qy 3361 AAATAAACAATAGGGTTCGCGCACATTTCCCGGAAAGTGCCACTGATCGGTGT 3420
Db 3087 AAATAAACAATAGGGTTCGCGCACATTTCCCGGAAAGTGCCACTGATCGGTGT 3146
Qy 3421 GAAATACCGCAGATGCGTAAGGAGAAATACCGCATCAGGAATTTGTAAGCGTTAATA 3480
Db 3147 GAAATACCGCAGATGCGTAAGGAGAAATACCGCATCAGGAATTTGTAAGCGTTAATA 3206
Qy 3481 ATTCAAGAACTCGTCAAGAGCGGATAGAGCGGATGCGCTCGAATCGGAGCGCG 3540
Db 3207 ATTCAAGAACTCGTCAAGAGCGGATAGAGCGGATGCGCTCGAATCGGAGCGCG 3266
Qy 3541 ATACCGTAAAGCAGAGGAAGCGGTTCAGCCCAATTCGCCCGCAAGCTCTTCAGCAATATCA 3600
Db 3267 ATACCGTAAAGCAGAGGAAGCGGTTCAGCCCAATTCGCCCGCAAGCTCTTCAGCAATATCA 3326
Qy 3601 CGGTAGCAAGCTATGCTCTGATAGCGGTTCGCCACACCCAGCGCGCACAGTCGATG 3660
Db 3327 CGGTAGCAAGCTATGCTCTGATAGCGGTTCGCCACACCCAGCGCGCACAGTCGATG 3386
Qy 3661 AATCAGAAAAAGCGCCATTTTCCACCATGATATTCCGCAAGCAGCATCGCATGGTGC 3720
Db 3387 AATCAGAAAAAGCGCCATTTTCCACCATGATATTCCGCAAGCAGCATCGCATGGTGC 3446
Qy 3721 ACGACGAGATCCTCGCGTTCGGGATGCTCGCTTGGAGCTTGGGAAACAGTTCGGCTGGC 3780
Db 3447 ACGACGAGATCCTCGCGTTCGGGATGCTCGCTTGGAGCTTGGGAAACAGTTCGGCTGGC 3506
Qy 3781 GCGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAGACCGGCTTCCATCGA 3840
Db 3507 GCGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAGACCGGCTTCCATCGA 3566
Qy 3841 GTACGTGCTCGTCCGATCGATGTTTTCGCTTGGTGGTGGTGGGAGTGGGATGAGCCGATCA 3900
Db 3567 GTACGTGCTCGTCCGATCGATGTTTTCGCTTGGTGGTGGTGGGAGTGGGATGAGCCGATCA 3626
Qy 3901 AGCGTATGAGCGCGCGCATTTGCATCAGCCATGATGGATCTTTCTCGGCAAGGCAAGG 3960
Db 3627 AGCGTATGAGCGCGCGCATTTGCATCAGCCATGATGGATCTTTCTCGGCAAGGCAAGG 3686
Qy 3961 TGAGATGACAGAGATCTTCCGCGCGGCTTCCGCAATAGCAGCGCTCCCTCCGCT 4020
Db 3687 TGAGATGACAGAGATCTTCCGCGCGGCTTCCGCAATAGCAGCGCTCCCTCCGCT 3746
Qy 4021 TCAGTGACAACTTCAGACACAGCTCGCAAGGAAACCGCGTCTGGCGAGCCAGCATAGC 4080
Db 3747 TCAGTGACAACTTCAGACACAGCTCGCAAGGAAACCGCGTCTGGCGAGCCAGCATAGC 3806
Qy 4081 CGCGTGCCTCGTCTTTGCAAGTTCAATTCAGGGCACCGGACAGCTCGGTCTTTGACAAAAAGA 4140
Db 3807 CGCGTGCCTCGTCTTTGCAAGTTCAATTCAGGGCACCGGACAGCTCGGTCTTTGACAAAAAGA 3866
Qy 4141 ACCGGCGCCCTTGCGCTGACAGCGGAAACAGCGGGCATCAGACGCGGATCTGCT 4200
Db 3867 ACCGGCGCCCTTGCGCTGACAGCGGAAACAGCGGGCATCAGACGCGGATCTGCT 3926
Qy 4201 TGTGCCCACTATAGCCGAATAGCTCTCCACCCAGCGCGCGGAGAACTCGCGTCAAT 4260
Db 3927 TGTGCCCACTATAGCCGAATAGCTCTCCACCCAGCGCGCGGAGAACTCGCGTCAAT 3986
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Qy 4261 CCATCTGTTCATCATCGGAAAGCATCTCATCTGTCTCTTCATCATCAGAGCTTGATCCC 4320
Db 3987 CCATCTGTTCATCATCGGAAAGCATCTCATCTGTCTCTTCATCATCAGAGCTTGATCCC 4046
Qy 4321 CTGCGCCATCAG 4332
Db 4047 CTGCGCCATCAG 4058

RESULT 5
US-10-811-028A-3
; Sequence 3, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Genteric, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-CAT
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-3

Query Match 54.1%; Score 2341.8; DB 8; Length 5753;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1971 AAAAAAANAANAACGGAATTCCTGAGCCCGGGGATCCACTAGTCTTAGAGCGGC 2030
Db 3392 ACAATAAATACTGTACGGAATTCCTGAGCCCGGGGATCCACTAGTCTTAGAGCGGC 3451
Qy 2031 CGCCACCGCGTGGAGCTCCAACTAGATGCAAGTGAATAAATGCTTTATTTGTGAAA 2090
Db 3452 CGCCACCGCGTGGAGCTCCAACTAGATGCAAGTGAATAAATGCTTTATTTGTGAAA 3511
Qy 2091 TTTGTGATGCTATTGCTTTTATTTGTAACTTAAAGCTGCAATAAACAAGTTAACACA 2150
Db 3512 TTTGTGATGCTATTGCTTTTATTTGTAACTTAAAGCTGCAATAAACAAGTTAACACA 3571
Qy 2151 ATTGCATTCAATTTATGTTTCAGGTTTTCAGGCGGAGGTGTGGAGGTTTTTTAAAGCCACA 2210
Db 3572 ATTGCATTCAATTTATGTTTCAGGTTTTCAGGCGGAGGTGTGGAGGTTTTTTAAAGCCACA 3631
Qy 2211 GCTCCAGCTTTTGTTCCTTTAGTTCAGGTTTAAATTTTCGAGCTTTCGCTTAATCATGCTCAT 2270
Db 3632 GCTCCAGCTTTTGTTCCTTTAGTTCAGGTTTAAATTTTCGAGCTTTCGCTTAATCATGCTCAT 3691
Qy 2271 AGCTGTTTCTGTGTGAATAATTTATCCGCTCAACAATTTCCACAAACATACGAGCCGGA 2330
Db 3692 AGCTGTTTCTGTGTGAATAATTTATCCGCTCAACAATTTCCACAAACATACGAGCCGGA 3751
Qy 2331 GCATAAAGTGAAGCTTGGGTCCTAATGATGAGCTAATCATTAATTTGGTTCG 2390
Db 3752 GCATAAAGTGAAGCTTGGGTCCTAATGATGAGCTAATCATTAATTTGGTTCG 3811
Qy 2391 GCTCACTCCCGCTTTTCCAGTCGGGAAACCTGCTGCTGCGAGCTGATTAATGAATCGGCC 2450
Db 3812 GCTCACTCCCGCTTTTCCAGTCGGGAAACCTGCTGCTGCGAGCTGATTAATGAATCGGCC 3871
Qy 2451 AACGCGCGGGAGAGCGGTTTTGCGTATTTGGCGCTCTTTCGCTCTCTGCTCACTGACT 2510
Db 3872 AACGCGCGGGAGAGCGGTTTTGCGTATTTGGCGCTCTTTCGCTCTCTGCTCACTGACT 3931
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-MC-CAT
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-4

Query Match	54.1%; Score 2341.8; DB 8; Length 5760;				
Best Local Similarity	99.4%; Pred. No. 0;				
Matches 2349; Conservative	0; Mismatches 13; Indels 0; Gaps 0;				
QY 1971	AAAAAAAAAAAAACGGAATCCCTGCACCGCGGGGATCCACTAGTCTTAGAGCGGC	2030			
DB 3399	ACAAATAAATATCTGTACGGAATTCCTGCACCGCGGGGATCCACTAGTCTTAGAGCGGC	3458			
QY 2031	CGCCACCGCGTGGAGCTCCACAACTAGAAATGCAATGAAAAAATGCTTTATTTGTGAAA	2090			
DB 3459	CGCCACCGCGTGGAGCTCCACAACTAGAAATGCAATGAAAAAATGCTTTATTTGTGAAA	3518			
QY 2091	TTTGTGATGCTATTGCTTTTATTTGTAACCATTTAAGCTGCAATTAACAAGTTTAACAACA	2150			
DB 3519	TTTGTGATGCTATTGCTTTTATTTGTAACCATTTAAGCTGCAATTAACAAGTTTAACAACA	3578			
QY 2151	ATTGCAATTCATTTATTTATGTTTTCAGGTTTCAGGGGAGGTCTGGAGGTTTTTTAAAGCCACA	2210			
DB 3579	ATTGCAATTCATTTATTTATGTTTTCAGGTTTCAGGGGAGGTCTGGAGGTTTTTTAAAGCCACA	3638			
QY 2211	GCTCCAGCTTTTGTTCCTTTAGTGTAGGTTTAAATTCGAGCTTGGCGTAAATCATGTCAT	2270			
DB 3639	GCTCCAGCTTTTGTTCCTTTAGTGTAGGTTTAAATTCGAGCTTGGCGTAAATCATGTCAT	3698			
QY 2271	AGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAACAATTCACACAACATACGAGCGGAA	2330			
DB 3699	AGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAACAATTCACACAACATACGAGCGGAA	3758			
QY 2331	GCATAAGTGTAAAGCTGGGTGCTTAATGATGAGCTTAATCACTCACTTAATTTGGTTGC	2390			
DB 3759	GCATAAGTGTAAAGCTGGGTGCTTAATGATGAGCTTAATCACTCACTTAATTTGGTTGC	3818			
QY 2391	GCTCACTGCCGCTTTCCAGTCCGGAAACCTGTCTGTCGAGCTGCAATTAATGAATCGGCC	2450			
DB 3819	GCTCACTGCCGCTTTCCAGTCCGGAAACCTGTCTGTCGAGCTGCAATTAATGAATCGGCC	3878			
QY 2451	AACGCGCGGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTTCTCGCTCACTGACT	2510			
DB 3879	AACGCGCGGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTTCTCGCTCACTGACT	3938			
QY 2511	CGCTCGCTCGCTCGTTCCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAATAC	2570			
DB 3939	CGCTCGCTCGCTCGTTCCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAATAC	3998			
QY 2571	GCTTATCCACAGAATCAGGGGATAACGCAAGGAAAGAACATGTGAGCAAAAGGCCAGCAA	2630			
DB 3999	GCTTATCCACAGAATCAGGGGATAACGCAAGGAAAGAACATGTGAGCAAAAGGCCAGCAA	4058			
QY 2631	AGGCCAGGAACGTTAAAGCGCGGTCTGCTGGCGTTTTTTCATAGGCTCCGCGCCCTG	2690			
DB 4059	AGGCCAGGAACGTTAAAGCGCGGTCTGCTGGCGTTTTTTCATAGGCTCCGCGCCCTG	4118			
QY 2691	ACGAGCATCAAAAAATCCAGCTCAAGTCAAGTGGCGGAAACCGCAGGACTATAAA	2750			
DB 4119	ACGAGCATCAAAAAATCCAGCTCAAGTGGCGGAAACCGCAGGACTATAAA	4178			
QY 2751	GATACAGCGGTTTCCCTGGAAGCTCCCTGTCGCGCTCTCTGTTTCCGACCTGCCGC	2810			
DB 4179	GATACAGCGGTTTCCCTGGAAGCTCCCTGTCGCGCTCTCTGTTTCCGACCTGCCGC	4238			
QY 2811	TTACCGGATACCTGTCGCGTTTCTCCCTTCGGAAGCTGGCGCTTCTCAATGCTCAC	2870			
DB 4239	TTACCGGATACCTGTCGCGTTTCTCCCTTCGGAAGCTGGCGCTTCTCAATGCTCAC	4298			
QY 2871	GCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAAGCTGGGCTGTGTGCAGAAC	2930			
DB 4299	GCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAAGCTGGGCTGTGTGCAGAAC	4358			

QY 2931	CCCCCGTTACGCGCAGCCGCTGGCCCTTATCCGGTAACTATCTCTTGTAGTCCCAACCGG	2990
DB 4359	CCCCCGTTACGCGCAGCCGCTGGCCCTTATCCGGTAACTATCTCTTGTAGTCCCAACCGG	4418
QY 2991	TAAGACACGACTTATCCCACTGGCAGCAGCACTGGTAAACAGGATTTAGCAGAGCGAGGT	3050
DB 4419	TAAGACACGACTTATCCCACTGGCAGCAGCACTGGTAAACAGGATTTAGCAGAGCGAGGT	4478
QY 3051	ATGTAGCGGTGTCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGA	3110
DB 4479	ATGTAGCGGTGTCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGA	4538
QY 3111	CAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTCGTAGCT	3170
DB 4539	CAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTCGTAGCT	4598
QY 3171	CTTCATCCGCAACAAACACCCGCTGCTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGA	3230
DB 4599	CTTCATCCGCAACAAACACCCGCTGCTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGA	4658
QY 3231	TTACGCGCAGAAAAAAGGATCTCAAGAAGATCTCTTTGATCTTTTCTACGGGGTCTGACG	3290
DB 4659	TTACGCGCAGAAAAAAGGATCTCAAGAAGATCTCTTTGATCTTTTCTACGGGGTCTGACG	4718
QY 3291	CTCAGTGAACCAAACTCACGTTTAAAGGATTTTGGTTCATGAGCGGATACATATTTGAAT	3350
DB 4719	CTCAGTGAACCAAACTCACGTTTAAAGGATTTTGGTTCATGAGCGGATACATATTTGAAT	4778
QY 3351	GTATTTAGAAAAATAAACAATAGGGTTCCGCGCACATTTTCCCGAAAAAGTCCACCTG	3410
DB 4779	GTATTTAGAAAAATAAACAATAGGGTTCCGCGCACATTTTCCCGAAAAAGTCCACCTG	4838
QY 3411	TATCGGTGTCAAAATACCGCACAGATGCTGAAGAGAAAAATACCCCATCAGGAAATTTGA	3470
DB 4839	TATCGGTGTCAAAATACCGCACAGATGCTGAAGAGAAAAATACCCCATCAGGAAATTTGA	4898
QY 3471	AGCGTTAATTTACAGAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCTGCGAATC	3530
DB 4899	AGCGTTAATTTACAGAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCTGCGAATC	4958
QY 3531	GGGAGCGCGATACCGTAAAGCACAGGAAGCGGTACGCCCATTCGCGCCCAAGCTCTTC	3590
DB 4959	GGGAGCGCGATACCGTAAAGCACAGGAAGCGGTACGCCCATTCGCGCCCAAGCTCTTC	5018
QY 3591	AGCAATATCAAGGTAGCAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGCGC	3650
DB 5019	AGCAATATCAAGGTAGCAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGCGC	5078
QY 3651	ACAGTCCGATGATCCAGAAAAAGCGCCATTTTCCACCATGATATTCGGCAAGCAGCATC	3710
DB 5079	ACAGTCCGATGATCCAGAAAAAGCGCCATTTTCCACCATGATATTCGGCAAGCAGCATC	5138
QY 3711	GCATGGGTTCACGACAGATCCTCGCGTCCGGCATGCTCGCTTTGAGCTCGCGAACAG	3770
DB 5139	GCATGGGTTCACGACAGATCCTCGCGTCCGGCATGCTCGCTTTGAGCTCGCGAACAG	5198
QY 3771	TTTCGCTGGCGGAGCGCCCTGATGCTCTTCGTCGAGATCATCTGATCGACAGACCGGC	3830
DB 5199	TTTCGCTGGCGGAGCGCCCTGATGCTCTTCGTCGAGATCATCTGATCGACAGACCGGC	5258
QY 3831	TTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTTCGCTTGGTGGTCCGAGGT	3890
DB 5259	TTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTTCGCTTGGTGGTCCGAGGT	5318
QY 3891	AGCCCGGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGATCTTTCTCGGC	3950
DB 5319	AGCCCGGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGATCTTTCTCGGC	5378
QY 3951	AGGAGCAAGGTGATGACGAGGATCTTCGCCCGCATTCGCCCAATAGCAGCGATC	4010
DB 5379	AGGAGCAAGGTGATGACGAGGATCTTCGCCCGCATTCGCCCAATAGCAGCGATC	5438
QY 4011	CCTTCCCGCTTTCAGTGACAAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCTGTCGCGCAG	4070

Db 5439 CCTTCCCGCTTCACTGCAACGTCGAGCAGAGTCGCGCAAGAACGCCCGCTCGTGGCCAG 5498
QY CCAGATAGCCGCGCTCGCTGCTTGCAGTTCAATTCAGGCGCAGGAGGTCGTCCT 4130
Db 5499 CCAGATAGCCGCGCTCGCTGCTTGCAGTTCAATTCAGGCGCAGGAGGTCGTCCT 5558
QY 4131 GACAAAAGAACCGGGGCGCCCTCGCTGAGCAGCGGAAACACGCGGCGCATCAGAGCAGCC 4190
Db 5559 GACAAAAGAACCGGGGCGCCCTCGCTGAGCAGCGGAAACACGCGGCGCATCAGAGCAGCC 5618
QY 4191 GATTGCTGTGTCGCCAGTCATAGCCGATAGCTCTCAACCACGCGGCGGAGAAC 4250
Db 5619 GATTGCTGTGTCGCCAGTCATAGCCGATAGCTCTCAACCACGCGGCGGAGAAC 5678
QY 4251 TGGCTGCAATCACTTGTTCATCATGCGGAAACGATCCTCATCTCTCTTGATCAGA 4310
Db 5679 TGGCTGCAATCCATCTTGTTCATCATGCGGAAACGATCCTCATCTCTCTTGATCAGA 5738
QY 4311 GCTTGATCCCTCGGCCATCAG 4332
Db 5739 GCTTGATCCCTCGGCCATCAG 5760

RESULT 7

US-10-234-406-3
; Sequence 3, Application US/10234406
; Publication No. US20030109478A1
; GENERAL INFORMATION:
; APPLICANT: FEWEL, Jason G.
; APPLICANT: MACLAUGHLIN, Fiona
; APPLICANT: SMITH, Louis C.
; APPLICANT: NICOL, Francois
; APPLICANT: ROLLAND, Alain
; TITLE OF INVENTION: NUCLEIC ACID FORMULATIONS FOR GENE DELIVERY AND METHODS OF USE
; FILE REFERENCE: 54964-8303.US01
; CURRENT APPLICATION NUMBER: US/10/234,406
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/187,236
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/261,751
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US01/06953
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3609
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression plasmid pEPl403 encoding for mouse erythropoietin (801)
; OTHER INFORMATION:) ... (1379)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (801)..(1379)
; OTHER INFORMATION:
US-10-234-406-3

Query Match 44.7%; Score 1937; DB 5; Length 3609;
Best Local Similarity 72.1%; Pred. No. 0;
Matches 2894; Conservative 0; Mismatches 626; Indels 492; Gaps 9;
QY 321 CGTTACATAACTTACGGTAAATGGCCCGCTCGGTGACCGGCCCAACGACCCCGCCCAT 380
Db 26 CGTTACATAACTTACGGTAAATGGCCCGCTCGGTGACCGGCCCAACGACCCCGCCCAT 85
QY 381 GACGTCATATAGCAGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTCA 440
Db 86 GACGTCATATAGCAGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTCA 145
QY 441 ATGGGTGGAGTATTACGGTAAATCGCCACTTGGCAGTACATCAAGTATCATATGCC 500

Db 146 ATGGGTGGAGTATTACGGTAAATCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 205
QY 501 AAGTAGCCCGCTTATGAGTCAATGACGTAATGCGCCCGCTGGCATTTATGCCAGTA 560
Db 206 AAGTAGCCCGCTTATGAGTCAATGACGTAATGCGCCCGCTGGCATTTATGCCAGTA 265
QY 561 CATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACGTATTAAGTATCGTATTAAC 620
Db 266 CATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACGTATTAAGTATCGTATTAAC 325
QY 621 CATGGTGAATCGCGTTTGGCAGTACATCAATGGGCGTGGATAGGGTTTGAATCAGCGGG 680
Db 326 CATGGTGAATCGCGTTTGGCAGTACATCAATGGGCGTGGATAGGGTTTGAATCAGCGGG 385
QY 681 ATTTCCAAAGTCTCCACCCCAATGACGTCATGGGAGTTTCTTTTGGCACCACAAATCAACG 740
Db 386 ATTTCCAAAGTCTCCACCCCAATGACGTCATGGGAGTTTCTTTTGGCACCACAAATCAACG 445
QY 741 GGACTTTTCCAAATGTGTAAACAATCCGCCCAATTTGACGCAAAATGGGCGGTAGCGGTGT 800
Db 446 GGACTTTTCCAAATGTGTAAACAATCCGCCCAATTTGACGCAAAATGGGCGGTAGCGGTGT 505
QY 801 ACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCTGGAGACG 860
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QY 981 TTAAGGAGCAATAGAAACTGGGCATGTGGAGACAGAGAAGACTCTTGGTTTCTGATA 1040
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QY 1041 GGCACGTACTCTCTGCTCTATTTTCCACCCCTTAGGCTGCTGCTGCTGAGCC 1100
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QY 1401 GCACACCGCGCGCTAGTGAACAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 1460
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D5 2125 AGAGTGGCGAAACCCGACAGGACTATAAAGATACACGAGCGTTTCCCTCGAAGCTCCC 2184
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D5 2696 ----- 2695
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D5 2696 ----- 2695
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D5 2696 -----TCAGAGAACTCTGTAAG 2713
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 DB 2651 ----- 2650
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Qy 3621 CTGATAGCGGTCCGCCACACCCAGCGCGCACAGTCGATGAATCCAGAAAGCGGCCATT 3680
Db 2789 CTGATAGCGGTCCGCCACACCCAGCGCGCACAGTCGATGAATCCAGAAAGCGGCCATT 2848
Qy 3681 TTCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAAGCAGAGATCCTCGCCGTC 3740
Db 2849 TTCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAAGCAGAGATCCTCGCCGTC 2908
Qy 3741 GGGCATCTCGCTTGAGCCCTGGCGAAGAGTTCGGCTGGCGAGCCCTGATGCTTTC 3800
Db 2909 GGGCATCGCGCCCTTGAGCCCTGGCGAAGAGTTCGGCTGGCGAGCCCTGATGCTTTC 2968
Qy 3801 GTCCAGATCATCTGATCGACAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCG 3860
Db 2969 GTCCAGATCATCTGATCGACAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCG 3028
Qy 3861 ATGTTTCGTTGGTGGTGAATGGCAGGATAGCGGATCAAGCGATGATGACAGGAGATCCTG 3920
Db 3029 ATGTTTCGTTGGTGGTGAATGGCAGGATAGCGGATCAAGCGATGATGACAGGAGATCCTG 3088
Qy 3921 TGATCAGCATGATGATGATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTG 3980
Db 3089 TGATCAGCATGATGATGATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTG 3148
Qy 3981 CCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAAGTGAACAGCTGAGCAC 4040
Db 3149 CCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAAGTGAACAGCTGAGCAC 3208
Qy 4041 AGCTGCGCAAGGAACCGCGTGTGGCCAGCAGATAGCGGCTGCTCGTCTGTCAG 4100
Db 3209 AGCTGCGCAAGGAACCGCGTGTGGCCAGCAGATAGCGGCTGCTCGTCTGTCAG 3268
Qy 4101 TTCAATTCAGGCAACCGGACAGTCTGTTGACAAAGAAACCGGCGCCCTGCGCTGA 4160
Db 3269 TTCAATTCAGGCAACCGGACAGTCTGTTGACAAAGAAACCGGCGCCCTGCGCTGA 3328
Qy 4161 CAGCGGAAACACCGCGGCATCAGAGCAGCGATGCTGTGTGCGCCAGTCAATAGCGAA 4220
Db 3329 CAGCGGAAACACCGCGGCATCAGAGCAGCGATGCTGTGTGCGCCAGTCAATAGCGAA 3388
Qy 4221 TAGCTCTCACCACGAGCGCGGAGAACTGGGTGCAATCTTGTTCATATGTCG 4280
Db 3389 TAGCTCTCACCACGAGCGCGGAGAACTGGGTGCAATCTTGTTCATATGTCG 3448
Qy 4281 AAACGATCTCATCTGCTCTTTCATCAGAGCTGATCCCTGGCCATCAG 4332
Db 3449 AAACGATCTCATCTGCTCTTTCATCAGATCTTGTATCCCTTGGCCATCAG 3500

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RESULT 10
 US-10-198-478-16
 ; Sequence 16, Application US/10198478
 ; Publication No. US2003018836A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Romano, Charles P.
 ; APPLICANT: Corbin, David R.
 ; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
 ; FILE REFERENCE: 38-21 (13547) B
 ; .CURRENT APPLICATION NUMBER: US/10/198,478

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; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
; NAME/KEY: misc feature
; LOCATION: (1)..(8349)
; OTHER INFORMATION:
US-10-198-478-16

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Query Match 42.6%; Score 1845.4; DB 6; Length 8349;
 Best Local Similarity 92.6%; Pred. No. 0;
 Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;

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Qy 2249 AGCTTGGCGTAAATCATGCTCATAGCTGTTTCCCTGTGTGAATTTGTTATCCGCTCACAAATT 2308
Db 5909 AGCTTGGCGTAAATCATGCTCATAGCTGTTTCCCTGTGTGAATTTGTTATCCGCTCACAAATT 5968
Qy 2309 CCACACAAATACATGAGCGGAGCAATAAAGTGTAAAGCCCTGGGTGCTTAATGAGTGAGC 2368
Db 5969 CCACACAAATACATGAGCGGAGCAATAAAGTGTAAAGCCCTGGGTGCTTAATGAGTGAGC 6028
Qy 2369 TAACTCACATTAATTCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGTC 2428
Db 6029 TAACTCACATTAATTCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGTC 6088
Qy 2429 CAGCTGCATTAATGAATTCGCGCAACCGCGGGGAGAGCGGTTTTCGTTATTTGGCGCTCT 2488
Db 6089 CAGCTGCATTAATGAATTCGCGCAACCGCGGGGAGAGCGGTTTTCGTTATTTGGCGCTCT 6148
Qy 2489 TCCGCTTCTTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2548
Db 6149 TCCGCTTCTTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 6208
Qy 2549 GCTCACTCAAGCGCGTAAATACCGTTATCCAGAAATACAGGGATTAACCGAGGAAAGAAC 2608
Db 6209 GCTCACTCAAGCGCGTAAATACCGTTATCCAGAAATACAGGGATTAACCGAGGAAAGAAC 6268
Qy 2609 ATGTGAGCAAAAGCGCGCAAAAGCGGAGCAACCGTAAAGGCGCGGTTTTCGTTATTTGGCGCTTT 2668
Db 6269 ATGTGAGCAAAAGCGCGCAAAAGCGGAGCAACCGTAAAGGCGCGGTTTTCGTTATTTGGCGCTTT 6328
Qy 2669 TTCCATAGGCTCCGCGCCCTCGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGG 2728
Db 6329 TTCCATAGGCTCCGCGCCCTCGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGG 6388
Qy 2729 CGAAACCCGACAGGATATAAAGATACAGGCGTTTCCCGCTTGGAGAGTCCCTCGTGGC 2788
Db 6389 CGAAACCCGACAGGATATAAAGATACAGGCGTTTCCCGCTTGGAGAGTCCCTCGTGGC 6448
Qy 2789 TCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGC 2848
Db 6449 TCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGC 6508
Qy 2849 GTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTTCGTTGAGGTGCTTCGCTCC 2908
Db 6509 GTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTTCGTTGAGGTGCTTCGCTCC 6568
Qy 2909 AAGCTGGCTGTGTGACGAAACCCCGCTTCAGCGGACCGCTGCGGCTTATTCGGTAAAC 2968
Db 6569 AAGCTGGCTGTGTGACGAAACCCCGCTTCAGCGGACCGCTGCGGCTTATTCGGTAAAC 6628
Qy 2969 TATCGTCTTGAAGTCCAAACCGGTAAGACACGACTTATCGCACCTGGCAGCAGCACCTGGT 3028
Db 6629 TATCGTCTTGAAGTCCAAACCGGTAAGACACGACTTATCGCACCTGGCAGCAGCACCTGGT 6688

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QY 3029 AACAGGATTAGCAGAGCAGGATATGTAGCGGTGCTACAGAGTTCTTTGAAGTGTGGCCT 3088
DB 6689 AACAGGATTAGCAGAGCAGGATATGTAGCGGTGCTACAGAGTTCTTTGAAGTGTGGCCT 6748
QY 3089 AACTACGGCTACACTAGAGACAGTATTTGGTATCTGGCGTCTGCTGAAGCCAGTTACC 3148
DB 6749 AACTACGGCTACACTAGAGACAGTATTTGGTATCTGGCGTCTGCTGAAGCCAGTTACC 6808
QY 3149 TTCGGAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGT 3208
DB 6809 TTCGGAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGT 6868
QY 3209 TTTTGTGTTTCAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCTCTTTG 3268
DB 6869 TTTTGTGTTTCAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCTCTTTG 6928
QY 3269 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTGGTC 3328
DB 6929 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTGGTC 6988
QY 3329 ATGAGCGGATACATATTTGAATGTATTTAGA----- 3359
DB 6989 ATGAGATTATCAAAAGGATCTTACCTAGATCTTTTGGGTGGCGAAGAACTCCAGC 7048
QY 3360 -----AAAATAACAAATAGGGTTTCCGGCACATTTCCCGAAG 3401
DB 7049 ATGAGATCCCGCGCTGGAGGATATCCAGCGCGCTCCCGAAGAAACGATTTCCGAAGCCC 7108
QY 3402 TGCCACCTGTATCGGTG-----TGAATACCGCACAGATGCGTAAAGGAGAAAT 3451
DB 7109 AACCTTTTCATAGAGGGCGGTGGAATCGAAATCTCGTATGGCAGTTGGGGTCGCT 7168
QY 3452 ACCGCATCAGGAAATTTGAAGCGTTTAAATTCAGAAGAACTCGTCAAGAAAGGCGATAGA 3511
DB 7169 TGGTCGTCATTTCGAACCCAGAGTCCGCTCAGAGAACTCGTCAAGAAAGGCGATAGA 7228
QY 3512 AGGCGATCGCTCGAAATCGGAGCGGCGATACCGTTAAAGCAACGAGGAAGCGGTGAGCCC 3571
DB 7229 AGGCGATCGCTCGAAATCGGAGCGGCGATACCGTTAAAGCAACGAGGAAGCGGTGAGCCC 7288
QY 3572 ATTCGCGCGCAAGCTTTTCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCCGT 3631
DB 7289 ATTCGCGCGCAAGCTTTTCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCCGT 7348
QY 3632 CGGCGACACCCAGCGCGCACAGTGCATGAATCCAGAAAAAGCGGCATTTTCCACCATGA 3691
DB 7349 CGGCGACACCCAGCGCGCACAGTGCATGAATCCAGAAAAAGCGGCATTTTCCACCATGA 7408
QY 3692 TATTCGGCAAGCAGGCATCGCCATGGGTCAACGAGATCTTCGCGCTCGGCGATGCTCG 3751
DB 7409 TATTCGGCAAGCAGGCATCGCCATGGGTCAACGAGATCTTCGCGCTCGGCGATGCTCG 7468
QY 3752 CTTTCAGCTGCGCAACAGTTTCGGCTGGCGGAGCCCTGATGCTCTTCGTCAGATCAT 3811
DB 7469 CTTTCAGCTGCGCAACAGTTTCGGCTGGCGGAGCCCTGATGCTCTTCGTCAGATCAT 7528
QY 3812 CTTTCAGCAAGACCGGCTTCCATCCGAGTAGTCTGCTCGATGCGATGTTTCGTT 3871
DB 7529 CTTTCAGCAAGACCGGCTTCCATCCGAGTAGTCTGCTCGATGCGATGTTTCGTT 7588
QY 3872 GGTGTTCGATGGCAGGTAGCCGATCAAGCGTATGACGCGCGCATTTGATCAGCA 3931
DB 7589 GGTGTTCGATGGCAGGTAGCCGATCAAGCGTATGACGCGCGCATTTGATCAGCA 7648
QY 3932 TGATGGATATTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGCGCATTT 3991
DB 7649 TGATGGATATTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGCGCATTT 7708
QY 3992 CGCCCAATAGCAGCAGTCCCTTCCGCTTTCAGTGAACAGTTCGAGCAACAGTTCGCGAAG 4051
DB 7709 CGCCCAATAGCAGCAGTCCCTTCCGCTTTCAGTGAACAGTTCGAGCAACAGTTCGCGAAG 7768
QY 4052 GAAACGCCGCTGTTGGCCACCGACGATAGCGCGCTGCTCTGTCAGTTTATTTCAGGG 4111

DB 7769 GAACGCCGCTGTTGGCCAGCAGATAGCCGCGTCTGCTCTGTCAGTTTCATTACGGG 7828
QY 4112 CACCGGACAGTGGTCTTGACAAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACA 4171
DB 7829 CACCGGACAGTGGTCTTGACAAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACA 7888
QY 4172 CGCGGCGATCAGAGCAGCCGATTTGTGTGTGCCAGTCATAGCCGAAATAGCTCTCCA 4231
DB 7889 CGCGGCGATCAGAGCAGCCGATTTGTGTGTGCCAGTCATAGCCGAAATAGCTCTCCA 7948
QY 4232 CCAGAGCGCGGAGAACCTGCGTGAATCCATCTCTTCAATCATCGAAACGATCTCTC 4291
DB 7949 CCCAAGCGCGGAGAACCTGCGTGAATCCATCTTGTTCATCATCGAAACGATCTCTC 8008
QY 4292 ATCTGTCTCTTGATCAGAGCTTGCATCCCTGCGCCATCAG 4332
DB 8009 ATCTGTCTCTTGATCAGATCTTGATCCCTGCGCCATCAG 8049

RESULT 11
US-10-841-796-33
; Sequence 33, Application US/10841796
; Publication No. US20040237138A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Biotechnology Corporation
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Nordine, Chiekh
; APPLICANT: Fisher, Dane
; APPLICANT: Thompson, Rebecca
; TITLE OF INVENTION: A method of increasing yield in a plant
; FILE REFERENCE: Docket number 38-21(15691)B
; CURRENT APPLICATION NUMBER: US/10/841.796
; CURRENT FILING DATE: 2004-07-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 11546
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid containing construct for corn transformation
US-10-841-796-33

Query Match 42.6%; Score 1845.4; DB 8; Length 11546;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;

QY 2249 AGCTTGGCGTAAATCATGTGTCATAGCTTTCTCTGTGTAATTTGTTATCCCGCTCACAATT 2308
DB 9106 AGCTTGGCGTAAATCATGTGTCATAGCTTTCTCTGTGTAATTTGTTATTTCCCGCTCACAATT 9165
QY 2309 CCACACAACTACAGCCGCGAAGCAATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGC 2368
DB 9166 CCACACAACTACAGCCGCGAAGCAATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGC 9225
QY 2369 TAACTCACTAAATTTGGTGGCTCACTGCCGCTTTCCAGTCGGAACCTGTCGTC 2428
DB 9226 TAACTCACTAAATTTGGTGGCTCACTGCCGCTTTCCAGTCGGAACCTGTCGTC 9285
QY 2429 CAGCTGCAATTAATGAATCGGCCAGCGCGGAGAGCGGTTTTCGCTATTGGGGGCTCT 2488
DB 9286 CAGCTGCAATTAATGAATCGGCCAGCGCGGAGAGCGGTTTTCGCTATTGGGGGCTCT 9345
QY 2489 TCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2548
DB 9346 TCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 9405
QY 2549 GCTCACTCAAGCGCGGTAAATCGGTTATCCACAGATCAGGGGTAACCCAGGAAAGAAC 2608
DB 9406 GCTCACTCAAGCGCGGTAAATCGGTTATCCACAGATCAGGGGTAACCCAGGAAAGAAC 9465
QY 2609 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGGTAAAGGCCGCTTGTGTCGCTTT 2668

[illegible]

Db 1569 AGCAAGTGTAGATGACAGGAGATCTGCCCCGACATTCGCCCAATAGCAGCCAGTCCCT 1628
Qy 4014 TCCCGCTTCAGTGACAGAGTGCAGACAGCTGCGCAAGGACGCCCTGTCGGCAGCCA 4073
Db 1629 TCCCGCTTCAGTGACAGAGTGCAGACAGCTGCGCAAGGACGCCCTGTCGGCAGCCA 1688
Qy 4074 CGATAGCGCGCTGCTGCTTTCAGTTCATTCAGGCGCACCGGACAGGTCTGTCGAC 4133
Db 1689 CGATAGCGCGCTGCTGCTTTCAGTTCATTCAGGCGCACCGGACAGGTCTGTCGAC 1748
Qy 4134 AAAAGAACCGGGCGCCCTGCTGCTGACAGCGGAAACAGCGCGCATCAGAGAGCCGAT 4193
Db 1749 AAAAGAACCGGGCGCCCTGCTGCTGACAGCGGAAACAGCGCGCATCAGAGAGCCGAT 1808
Qy 4194 TGTCTGTTGTGCCAGTCATAGCCGATAGCTCTCCACCCAGCGCGGAGAACCTGC 4253
Db 1809 TGTCTGTTGTGCCAGTCATAGCCGATAGCTCTCCACCCAGCGCGGAGAACCTGC 1868
Qy 4254 GTGCAATCCATCTTGTTCATCATCGGAAACGATCCTCATCTGCTCTTGTATCAGAGCT 4313
Db 1869 GTGCAATCCATCTTGTTCATCATCGGAAACGATCCTCATCTGCTCTTGTATCAGATCT 1928
Qy 4314 TGATCCCTCGGCCATCAG 4332
Db 1929 TGATCCCTCGGCCATCAG 1947

RESULT 13
US-10-021-403A-10
; Sequence 10, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
; APPLICANT: Adviseys
; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhance
; TITLE OF INVENTION: Growth in Offspring
; FILE REFERENCE: HO-P02021US1/100021476/OTA 00-91
; CURRENT APPLICATION NUMBER: US/10/021.403A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/255,021
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone
US-10-021-403A-10

Query Match 39.7%; Score 1718.4; DB 5; Length 2192;
Best Local Similarity 90.5%; Pred. No. 0; Mismatches 11; Indels 191; Gaps 1;
Matches 1926; Conservative 0;
; Qy 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT 2264
Db 24 GGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT 83
Qy 2265 GGTCTATAGCTGTTTCTGTTGTAATTTGTTATCGCTCACAATTCACACAAATACGAG 2324
Db 84 GGTCTATAGCTGTTTCTGTTGTAATTTGTTATCGCTCACAATTTCCACAAATACGAG 143
Qy 2325 CCGGAAGCATAAAGTGTAAAGCTTGGGGTGGCTTAATGAGTGAGCTAACTCACATTAAATG 2384
Db 144 CCGGAAGCATAAAGTGTAAAGCTTGGGGTGGCTTAATGAGTGAGCTAACTCACATTAAATG 203
Qy 2385 CGTTGCGCTCACTGCCCGCTTTTCAGTTCGGGAAACCTGTGTCGCGAGCTGCATTAATGAA 2444
Db 204 CGTTGCGCTCACTGCCCGCTTTTCAGTTCGGGAAACCTGTGTCGCGAGCTGCATTAATGAA 263
Qy 2445 TCGCCCAACCGCGGGAGAGGGTTTGGTATTTGGGCGCTCTTCGCTTCCTCGCTCA 2504

Db 264 TCGGCCAAACGCGCGGAGAGCGGTTTGGGTATTTGGGCGCTCTTTCGCTTCTCGCTCA 323
Qy 2505 CTGACTCGCTGCGCTCGGTTGCTTGGCTGCGGCGAGGGGTATCAGCTCACTCAAAAGCGG 2564
Db 324 CTGACTCGCTGCGCTCGGTTGCTTGGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 383
Qy 2565 TAATAAGGTTATCCACAGATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCC 2624
Db 384 TAATAAGGTTATCCACAGATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCC 443
Qy 2625 AGCAAAAGGCGCAGAACCGTAAAGAGCCGCTTGTGCGGTTTTCATAGGTCGCGC 2684
Db 444 AGCAAAAGGCGCAGAACCGTAAAGAGCCGCTTGTGCGGTTTTCATAGGTCGCGC 503
Qy 2685 CCCCTGACGAGCATCAGAAATCGAGCTCAAGTCAAGAGTGGCGGAAACCGCAGAGAC 2744
Db 504 CCCCTGACGAGCATCAGAAATCGAGCTCAAGTCAAGAGTGGCGGAAACCGCAGAGAC 563
Qy 2745 TATAAAGATACAGGGGTTTCCCTCGGAAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 2804
Db 564 TATAAAGATACAGGGGTTTCCCTCGGAAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 623
Qy 2805 TGCCTGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAAT 2864
Db 624 TGCCTGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAT 683
Qy 2865 GCTCAGCTGTAGTATCTCAGTTCGCTGAGTTCGCTTCCCTTCGGAAGCGTGGCGCTTCTGTC 2924
Db 684 GCTCAGCTGTAGTATCTCAGTTCGCTGAGTTCGCTTCCCTTCGGAAGCGTGGCGCTTCTGTC 743
Qy 2925 ACGAACCCCTGTTACGCGCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCA 2984
Db 744 ACGAACCCCTGTTACGCGCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCA 803
Qy 2985 ACCCGTACAGACAGCTTATCCGCTGCGCAGCAGCTTATCGCTGAGTACAGATTAGCAGAG 3044
Db 804 ACCCGTACAGACAGCTTATCCGCTGCGCAGCAGCTTATCGCTGAGTACAGATTAGCAGAG 863
Qy 3045 CGAGGTATGTAGCGGTGCTACAGAGTTCCTTGAAGTGGTGGCTTAACCTACGCTTACACTA 3104
Db 864 CGAGGTATGTAGCGGTGCTACAGAGTTCCTTGAAGTGGTGGCTTAACTACGCTTACACTA 923
Qy 3105 GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTG 3164
Db 924 GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTG 983
Qy 3165 GTAGCTCTTGATCCGCAACAAACCCGCTGCTAGCGGTGTTTTCCTGTTGTCGAGC 3224
Db 984 GTAGCTCTTGATCCGCAACAAACCCGCTGCTAGCGGTGTTTTCCTGTTGTCGAGC 1043
Qy 3225 AGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTCTTGATCTTTTCTACGCGGT 3284
Db 1044 AGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTCTTGATCTTTTCTACGCGGT 1103
Qy 3285 CTGACGCTCAGTGGAAACGAAACTACGTTTAAAGGATTTTGGTCATGAGCGGATACATAT 3344
Db 1104 CTGACGCTTAAAGGATTTTGGTCATGAGCGGATACATAT 3344
Qy 3345 TTGAATGTATTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAAAGTGC 3404
Db 1111 TTGAATGTATTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAAAGTGC 1110
Qy 3405 CACCTGTATCGGTTGTAATAATCCGACAGATCGCTAAGGAGAAAAATACCGCATCAGAA 3464
Db 1111 CACCTGTATCGGTTGTAATAATCCGACAGATCGCTAAGGAGAAAAATACCGCATCAGAA 1110
Qy 3465 ATTGTAAGCGTTAAATTTCAAGAAACTCGTCAAGAGCGGATAGAGCGGATGCGCTG 3524
Db 1111 ATTGTAAGCGTTAAATTTCAAGAAACTCGTCAAGAGCGGATAGAGCGGATGCGCTG 1152
Qy 3525 CGAATCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTACGCCATTTCCCGGCCAAG 3584
Db 1153 CGAATCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTACGCCATTTCCCGGCCAAG 1212

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QY 3585 CTCTTACGCAATATACGGGTAGCAACGGCTATGTCTGTATAGCGGTCCGCCACACCCAG 3644
Db 1213 CTCCTTACGCAATATACGGGTAGCAACGGCTATGTCTGTATAGCGGTCCGCCACACCCAG 1272
QY 3645 CCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 3704
Db 1273 CCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 1332
QY 3705 GGCATCGCATGGGTACAGACGAGATCCTCCCGTCGGGCATGTCTCGCTTGGAGCTGGC 3764
Db 1333 GGCATCGCCATGGGTACAGACGAGATCCTCCCGTCGGGCATGTCTCGCTTGGAGCTGGC 1392
QY 3765 GAACAGTTTCGGCTGGCGGAGCCCTGTATGCTCTTCGTCAGATCATCTCTGATCGACAAG 3824
Db 1393 GAACAGTTTCGGCTGGCGGAGCCCTGTATGCTCTTCGTCAGATCATCTCTGATCGACAAG 1452
QY 3825 ACCGGCTTCATCCGAGTACGTCTCGCTCGATCGGATGTTTCGGTTGGTTCGATGG 3884
Db 1453 ACCGGCTTCATCCGAGTACGTCTCGCTCGATCGGATGTTTCGGTTGGTTCGATGG 1512
QY 3885 GCAGTACCCGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGGATCTTT 3944
Db 1513 GCAGTACCCGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGGATCTTT 1572
QY 3945 CTCGSCAGGACAGGTGAGATGACAGAGATCTCTGCCCCGCACTTCGCCCAATAGCAG 4004
Db 1573 CTCGSCAGGACAGGTGAGATGACAGAGATCTCTGCCCCGCACTTCGCCCAATAGCAG 1632
QY 4005 CCAGTCCCTTCCCGCTTCAGTGACAAAGTCGAGACAGCTCGGCAAGAAAGCCCGTCGT 4064
Db 1633 CCAGTCCCTTCCCGCTTCAGTGACAAAGTCGAGACAGCTCGGCAAGAAAGCCCGTCGT 1692
QY 4065 GSCCAGCCACGATAGCCGCTGCTCTGTCAGATTCATTCAGGGCACCGGACAGGTC 4124
Db 1693 GSCCAGCCACGATAGCCGCTGCTCTGTCAGATTCATTCAGGGCACCGGACAGGTC 1752
QY 4125 GGTCTTGACAAAGAAACCGGGCGCCCTGGCTGACAGCGGAAACACGGCGGCATCAGA 4184
Db 1753 GGTCTTGACAAAGAAACCGGGCGCCCTGGCTGACAGCGGAAACACGGCGGCATCAGA 1812
QY 4185 GCAGCCGATGTCTGTGTCGCTCATAGCCGATAGCCCTCTCCACCCAGCGGCCGG 4244
Db 1813 GCAGCCGATGTCTGTGTCGCTCATAGCCGATAGCCCTCTCCACCCAGCGGCCGG 1872
QY 4245 AGAACCCTGCTGCAATCCATCTTGTTCATCATGCGAAACGATCCTCATCTCTCTTG 4304
Db 1873 AGAACCCTGCTGCAATCCATCTTGTTCATCATGCGAAACGATCCTCATCTCTCTTG 1932
QY 4305 ATCAGAGCTTGATCCCTGCGCCATCAG 4332
Db 1933 ATCAGATCTTGATCCCTGCGCCATCAG 1960

RESULT 14
US-10-136-837-2
; Sequence 2, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTROM, Jeffrey L
; APPLICANT: PERICLE, Federica
; APPLICANT: ROLLAND, Alain
; APPLICANT: RALSTON, Robert
; TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 273/082 (GM15-1USC1)
; CURRENT APPLICATION NUMBER: US/10/136,837
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/268,135
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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; LENGTH: 3426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse Interferon Alpha pIF0826
US-10-136-837-2

Query Match      39.7%; Score 1718.4; DB 6; Length 3426;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

QY 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTTTCGAGCTTGGCGTAATCAT 2264
Db 793 GGCCTGGTACAGCTTTTGTTCCTTTAGTGAGGGTTAAATTTTCGAGCTTGGCGTAATCAT 852
QY 2265 GGTATAGCTGTTCCTGTGTGAAATTTTATCCGCTCACAAATTCACACAAACATACGAG 2324
Db 853 GGTATAGCTGTTCCTGTGTGAAATTTTATCCGCTCACAAATTCACACAAACATACGAG 912
QY 2325 CCGAAGCATAAAGTGTAAAGCCTTGGGTGCTTAATGAGTCAGCTTAATCATTAATTTG 2384
Db 913 CCGAAGCATAAAGTGTAAAGCCTTGGGTGCTTAATGAGTCAGCTTAATCATTAATTTG 972
QY 2385 GATTGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTCTGTGCGAGCTGCATTAATGAA 2444
Db 973 GATTGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTCTGTGCGAGCTGCATTAATGAA 1032
QY 2445 TCGGCCAAACGCGCGGGGAGAGCGGTTTGTGTATGTTGGCGCTCTTTCGCTTCCTCGCTCA 2504
Db 1033 TCGGCCAAACGCGCGGGGAGAGCGGTTTGTGTATGTTGGCGCTCTTTCGCTTCCTCGCTCA 1092
QY 2505 CTGACTCGCTCGCTCGCTCGCTTCGGCTGCGGCGAGCGGTATCAGCTCACATCAAGGCGG 2564
Db 1093 CTGACTCGCTCGCTCGCTCGCTTCGGCTGCGGCGAGCGGTATCAGCTCACATCAAGGCGG 1152
QY 2565 TAATACGCTTATCCACAGAAATCAGGGGATAACCGAGGAAAGAAACATGTGAGCAAAAGGCC 2624
Db 1153 TAATACGCTTATCCACAGAAATCAGGGGATAACCGAGGAAAGAAACATGTGAGCAAAAGGCC 1212
QY 2625 AGCAAAAGGCCAGGAAACCGTAAAAAGCGCGTTGTCTGGCGCTTTTTCATAGGCTCCGCC 2684
Db 1213 AGCAAAAGGCCAGGAAACCGTAAAAAGCGCGTTGTCTGGCGCTTTTTCATAGGCTCCGCC 1272
QY 2685 CCCCTGACGAGCATCACAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGGAC 2744
Db 1273 CCCCTGACGAGCATCACAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGGAC 1332
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Db 1333 TATAAAGATACGAGCGGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCGACCC 1392
QY 2805 TGCCGCTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGGCTTTCTCAAT 2864
Db 1393 TGCCGCTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGGCTTTCTCATA 1452
QY 2865 GCTACGCTGTAGGTATCTCAGTTCGFTAGTGTAGTTCGCTCCAGCTGGGCTGTGTGC 2924
Db 1453 GCTACGCTGTAGGTATCTCAGTTCGFTAGTGTAGTTCGCTCCAGCTGGGCTGTGTGC 1512
QY 2925 ACGAAACCCCCCGTTTCAGGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTGTAGTCCA 2984
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QY 2985 ACCCGGTAAAGACACAGACTTATCCCACTGGCAGAGCCACTGTAAACAGGATAGCAGAG 3044
Db 1573 ACCCGGTAAAGACACAGACTTATCCCACTGGCAGAGCCACTGTAAACAGGATAGCAGAG 1632
QY 3045 CGAGGTATGTAGCGGTGCTACAGAGTCTTCAAGTGTGGTGGCTTAACCTACGGCTACACTA 3104
Db 1633 CGAGGTATGTAGCGGTGCTACAGAGTCTTCAAGTGTGGTGGCTTAACCTACGGCTACACTA 1692
QY 3105 GAAGGACAGTATTTGGTATCTCGCTGCTGAAAGCAAGTTTACCTTCGGAAGAAAGAGTTG 3164
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Db 1693 GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAAAGAGTTG 1752
 Qy 3165 GTAGCTCTTGATCCGGCAACAAACACCGCTGCTAGCGGTGTTTCTTTGTTGCAAGC 3224
 Db 1753 GTAGCTCTTGATCCGGCAACAAACACCGCTGCTAGCGGTGTTTCTTTGTTGCAAGC 1812
 Qy 3225 AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTCTTTGATCTTTTCTACGGGGT 3284
 Db 1813 AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTCTTTGATCTTTTCTACGGGGT 1872
 Qy 3285 CTGAGCGCTCAGTGGAACGAAACATCAGTTAAGGATTTTGGTCATGAGCGGATACATAT 3344
 Db 1873 CTGAGCG----- 1879
 Qy 3345 TTGAATGTATTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGGAAAGTGC 3404
 Db 1880 ----- 1879
 Qy 3405 CACCTGTATGCGGTGTAATAACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGAA 3464
 Db 1880 ----- 1879
 Qy 3465 ATTGTAAGCGTTAATAATTGAGAAGAACTGCTCAAGAAAGCGATAGAAAGCGGATGCGCTG 3524
 Db 1880 -----TCAAGAAAGTCTGCTCAAGAAAGCGATAGAAAGCGGATGCGCTG 1921
 Qy 3525 CGAATCGGAGCGCGATACCGTAAAGCAGGAGAGCGGTCAAGCCCATTCGCGCCCAAG 3584
 Db 1922 CGAATCGGAGCGCGATACCGTAAAGCAGGAGAGCGGTCAAGCCCATTCGCGCCCAAG 1981
 Qy 3585 CTCTTCAGCAATATCACGGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG 3644
 Db 1982 CTCTTCAGCAATATCACGGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG 2041
 Qy 3645 CCGGCCACAGTCAGTGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 3704
 Db 2042 CCGGCCACAGTCAGTGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 2101
 Qy 3705 GGCATCGCCATGGGTACAGCAGAGATCTCGCCGTGCGGGATGCTCGCCCTTGAGCCCTGGC 3764
 Db 2102 GGCATCGCCATGGGTACAGCAGAGATCTCGCCGTGCGGGATGCTCGCCCTTGAGCCCTGGC 2161
 Qy 3765 GAACAGTTGCGGTGCGCGAGCCCTGATGCTCTGCTCAGATCATCTCTGATGCAAG 3824
 Db 2162 GAACAGTTGCGGTGCGCGAGCCCTGATGCTCTCTGCTCAGATCATCTCTGATGCAAG 2221
 Qy 3825 ACCGGCTTCATCCGAGTACGTGCTCGCTCGATGCGATGTTTGGTGGTGGTGGTGGTGGT 3884
 Db 2222 ACCGGCTTCATCCGAGTACGTGCTCGCTCGATGCGATGTTTGGTGGTGGTGGTGGTGGT 2281
 Qy 3885 GCAGGTAGCCGATCAAGCGTATGACCGCGCATTTGATGATGATGATGATGATGATGATGAT 3944
 Db 2282 GCAGGTAGCCGATCAAGCGTATGACCGCGCATTTGATGATGATGATGATGATGATGATGAT 2341
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 Db 2342 CTCGGCAGGAGCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2401
 Qy 4005 CCAGTCCCTTCCCGCTTCAGTGACAGCTGAGCAGAGCTGCGGCAAGGAGCGCGCTCGT 4064
 Db 2402 CCAGTCCCTTCCCGCTTCAGTGACAGCTGAGCAGAGCTGCGGCAAGGAGCGCGCTCGT 2461
 Qy 4065 GGCAGCCAGATAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4124
 Db 2462 GGCAGCCAGATAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2521
 Qy 4125 GGTCTTGACAAAAGAAACCGGGGCGCCCTCGCTGATGACAGCGGAAACAGCGCGGATCAGA 4184
 Db 2522 GGTCTTGACAAAAGAAACCGGGGCGCCCTCGCTGATGACAGCGGAAACAGCGCGGATCAGA 2581
 Qy 4185 GCAGCCGATGCTGTTGTCGCCAGTCATAGCCGATAGCTCTCCACCCAGCGCGCG 4244
 Db 2582 GCAGCCGATGCTGTTGTCGCCAGTCATAGCCGATAGCTCTCCACCCAGCGCGCG 2641

Qy 4245 AGAACCTGCGTCAATCCCATCTTGTCAATCATCGGAACGATCCTCATCTCTCTCTTG 4304
 Db 2642 AGAACCTGCGTCAATCCCATCTTGTCAATCATCGGAACGATCCTCATCTCTCTCTTG 2701
 Qy 4305 ATCAGAGCTTGTATCCCTCGCCCATCAG 4332
 Db 2702 ATCAGATCTTGTATCCCTCGCCCATCAG 2729

RESULT 15

US-10-021-403A-9
 ; Sequence 9, Application US/10021403A
 ; Publication No. US20030074679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Advisys
 ; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhance
 ; FILE REFERENCE: Growth in Offspring
 ; CURRENT APPLICATION NUMBER: US/10/021,403A
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/255,021
 ; PRIOR FILING DATE: 2000-12-12
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: This is a plasmid pSPC5-12-HVHRH utilized in the present invention
 ; OTHER INFORMATION: on.
 US-10-021-403A-9

Query Match 39.7%; Score 1718.4; DB 5; Length 3534;
 Best Local Similarity 90.5%; Pred. No. 0;
 Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

Qy 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTGGGTTAATTTTCGAGCTTCGCGTAATCAT 2264
 Db 1366 GGCCTGATCCAGCTTTTGTTCCTTTAGTGGGTTAATTTTCGAGCTTCGCGTAATCAT 1425
 Qy 2265 GGTATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCACAATTTCCACACATACGAG 2324
 Db 1426 GGTATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCACAATTTCCACACATACGAG 1485
 Qy 2325 CCGAAGCATAAAGTGAAGCTGGGGTCTTAATGAGTGAAGTAACTCAATTAATG 2384
 Db 1486 CCGAAGCATAAAGTGAAGCTGGGGTCTTAATGAGTGAAGTAACTCAATTAATG 1545
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 Qy 2445 TCGGCCAACCGCGGGGAGAGCGGTTTGGTATTGGGGGCTCTTCCGCTTCCTCGCTCA 2504
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 Qy 2505 CTGACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2564
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 Db 1846 CCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGGAC 1905

Qy	2745	TATAAGATACCGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC	2804
Db	1906	TATAAGATACCGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC	1965
Qy	2805	TGCGCTTACCGGATACCTGTCGCCCTTTCCTTCGGGAAGCGTGGCGCTTCTCAAT	2864
Db	1966	TGCGCTTACCGGATACCTGTCGCCCTTTCCTTCGGGAAGCGTGGCGCTTCTCAAT	2025
Qy	2865	GCTCAGCGTAGGTATCTCAGTTCGGGTAGGTGCTTCGCTCCAAAGCTGGCTGTGTC	2924
Db	2026	GCTCAGCGTAGGTATCTCAGTTCGGGTAGGTGCTTCGCTCCAAAGCTGGCTGTGTC	2085
Qy	2925	ACGAACCCCGTTTCAGCGCCGCTGCGCTTATCCGGTAACTATCGTCTTCAGTCCA	2984
Db	2086	ACGAACCCCGTTTCAGCGCCGCTGCGCTTATCCGGTAACTATCGTCTTCAGTCCA	2145
Qy	2985	ACCGGTTAAGACACGACTTATCGGCACTGGGAGGAGCCACTGGTAAACGAGTTAGCAG	3044
Db	2146	ACCGGTTAAGACACGACTTATCGGCACTGGGAGGAGCCACTGGTAAACGAGTTAGCAG	2205
Qy	3045	CGAGGTATGAGGCGTCTACAGAGTCTTGAAGTGGTGGCTTAACTACGCTACACTA	3104
Db	2206	CGAGGTATGAGGCGTCTACAGAGTCTTGAAGTGGTGGCTTAACTACGCTACACTA	2265
Qy	3105	GAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG	3164
Db	2266	GAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG	2325
Qy	3165	GTAGCTCTTGATTCGGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTGTTGCAAGC	3224
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Qy	3225	AGCAGATTACCGCGAAGAAAGATCTCAAGAGATCCTTTGATCTTTCTACGGGT	3284
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Qy	3285	CTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGGTCATGACGCGATACATAT	3344
Db	2446	CTGACGC-----	2452
Qy	3345	TTGAATGATTTTAGAAAAATAAAATAAGGGTTTCGGGCACATTTCCCGAAAAAGTGC	3404
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Qy	3405	CACCTGTATGCGGTGTAATACCGCACAGATGCGTAAGGAGAAATACCGCATCAGGAA	3464
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Qy	3585	CTCTTCAGCAATATCACGGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG	3644
Db	2555	CTCTTCAGCAATATCACGGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG	2614
Qy	3645	CCGGCCACAGTCGATGAATCCAGAAAGCGGCGATTTTCCACATGATATTCGGCAAGCA	3704
Db	2615	CCGGCCACAGTCGATGAATCCAGAAAGCGGCGATTTTCCACATGATATTCGGCAAGCA	2674
Qy	3705	GGCCTCGCATGGGTCCAGCGAGATCCTCGCGTCGGGATGCTCGCTTGAGCCTGGC	3764
Db	2675	GGCCTCGCATGGGTCCAGCGAGATCCTCGCGTCGGGATGCTCGCGCTTGAGCCTGGC	2734
Qy	3765	GAAACGTTCCGGTGGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAG	3824
Db	2735	GAAACGTTCCGGTGGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAG	2794

Qy	3825	ACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTTGGTGGTCAATGG	3884
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Qy	3885	GCAGGTAGCCGGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGATACTTT	3944
Db	2855	GCAGGTAGCCGGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGATACTTT	2914
Qy	3945	CTCGGAGGAGCAAGGTGAGATGACAGGAGATCTGCCCCGGCACCTTCGCCCAATAGCAG	4004
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Qy	4005	CCAGTCCCTTCCCGCTTCAGTGACAAGCTCGAGCACAGCTGCGCAAGGAGCGCCCGT	4064
Db	2975	CCAGTCCCTTCCCGCTTCAGTGACAAGCTCGAGCACAGCTGCGCAAGGAGCGCCCGT	3034
Qy	4065	GGCCAGCCACGATAGCCGCTGCTGCTCTTGAGTTCATTTCAGGGCACCCGACAGGTC	4124
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Qy	4125	GGTCTTGACAAAAAGAAACCGGGCGCCCTGCGTGAACGCGGGAACACGGCGGCATCAGA	4184
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Qy	4185	GCAGCCGATTGTCTGTTGTGCCCCAGTCATAGCCGAATAGCTCTCCACCCAAAGCGCGG	4244
Db	3155	GCAGCCGATTGTCTGTTGTGCCCCAGTCATAGCCGAATAGCTCTCCACCCAAAGCGCGG	3214
Qy	4245	AGAACCTGCGTGAATCCATCTTGTTCATCATCGGAAACGATCCTCATCTCTCTTTG	4304
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Qy	4305	ATCAGAGCTTGATCCCTCGGCCATCAG	4332
Db	3275	ATCAGATCTTGATCCCTCGGCCATCAG	3302

Search completed: March 15, 2006, 21:00:20
Job time : 3019 secs

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 20:54:32 ; Search time 1189 Seconds
(without alignments)
8495.331 Million cell updates/sec

Title: US-10-811-028A-1

Perfect score: 4331

Sequence: 1 cggtgaggcctcttcgcta.....ttgatccctgcgcacatcag 4332

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1718.4	39.7	3534	7 US-10-764-818A-11	Sequence 11, Appl
2	1718.4	39.7	3534	7 US-10-764-818A-12	Sequence 12, Appl
3	1718.4	39.7	3534	7 US-10-764-818A-13	Sequence 13, Appl
4	1718.4	39.7	3534	7 US-10-764-818A-14	Sequence 14, Appl
5	1718.4	39.7	3534	7 US-10-764-818A-15	Sequence 15, Appl
6	1718.4	39.7	3534	7 US-10-764-818A-22	Sequence 22, Appl
7	1718.4	39.7	3534	12 US-11-186-282-22	Sequence 22, Appl
8	1718.4	39.7	4855	7 US-10-764-818A-27	Sequence 27, Appl
9	1718.4	39.7	3558	7 US-10-764-818A-26	Sequence 26, Appl
10	1604.2	37.0	5181	12 US-11-094-484-3	Sequence 3, Appl
11	1457.8	33.7	2722	12 US-11-186-282-23	Sequence 23, Appl
12	1457.8	33.7	2725	12 US-11-186-282-24	Sequence 24, Appl
13	1456.2	33.6	2700	12 US-11-186-282-33	Sequence 33, Appl
14	1456.2	33.6	2716	7 US-10-764-818A-19	Sequence 19, Appl
15	1456.2	33.6	2716	7 US-10-764-818A-20	Sequence 20, Appl
16	1456.2	33.6	2716	12 US-11-186-282-27	Sequence 27, Appl
17	1456.2	33.6	2716	12 US-11-186-282-28	Sequence 28, Appl
18	1456.2	33.6	2716	12 US-11-186-282-29	Sequence 29, Appl
19	1456.2	33.6	2716	12 US-11-186-282-31	Sequence 31, Appl
20	1456.2	33.6	2721	12 US-11-186-282-26	Sequence 26, Appl

21	1456.2	33.6	2721	12 US-11-186-282-34	Sequence 34, Appl
22	1456.2	33.6	2725	7 US-10-764-818A-30	Sequence 30, Appl
23	1456.2	33.6	2725	12 US-11-186-282-25	Sequence 25, Appl
24	1456.2	33.6	2725	12 US-11-186-282-32	Sequence 32, Appl
25	1456.2	33.6	2739	7 US-10-764-818A-28	Sequence 28, Appl
26	1456.2	33.6	2739	12 US-11-186-282-30	Sequence 30, Appl
27	1397.6	32.3	5225	12 US-11-231-725-1	Sequence 1, Appl
28	1339.2	30.9	6233	12 US-11-193-750-10	Sequence 10, Appl
29	1294.8	29.9	4432	12 US-11-115-425-12	Sequence 12, Appl
30	1294.8	29.9	4864	12 US-11-115-425-14	Sequence 14, Appl
31	1274.4	29.4	2403	7 US-10-523-682-1	Sequence 1, Appl
32	1197.2	27.6	4886	12 US-11-005-216-4	Sequence 4, Appl
33	1197.2	27.6	4151	12 US-11-213-368-15	Sequence 15, Appl
34	1197.2	27.6	4181	12 US-11-170-123-1	Sequence 1, Appl
35	1197.2	27.6	4183	12 US-11-170-123-2	Sequence 2, Appl
36	1197.2	27.6	4692	12 US-11-082-154A-29	Sequence 29, Appl
37	1197.2	27.6	4862	12 US-11-082-154A-87	Sequence 87, Appl
38	1197.2	27.6	4894	12 US-11-181-148-2	Sequence 2, Appl
39	1197.2	27.6	7487	12 US-11-181-148-4	Sequence 4, Appl
40	1195.4	27.6	3913	8 US-10-981-267-27	Sequence 27, Appl
41	1189.2	27.5	4732	12 US-11-145-532-8	Sequence 8, Appl
42	1179.8	27.2	4710	12 US-11-131-479-92	Sequence 92, Appl
43	1179.4	27.2	7765	12 US-11-131-479-110	Sequence 110, App
44	1179.4	27.2	7765	12 US-11-131-479-111	Sequence 111, App
45	1174.6	27.1	2710	7 US-10-764-818A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-764-818A-11
; Sequence 11, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES C
; TITLE OF INVENTION: HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVS1-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the HV-GHRH plasmid.
US-10-764-818A-11

Query Match	39.7%	Score 1718.4	DB 7	Length 3534
Best Local Similarity	90.5%	Pred No. 7.5e-235		
Matches 1926	Conservative 0	Mismatches 11	Indels 191	Gaps 1
Qy	2205	GCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT	2264	
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Qy	2265	GGTCATAGCTTTTCTGTGTGAATTTATTCGCTCACAANTTCCACACATACGAG	2324	
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Qy	2325	CCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGTAACTCACAATTAATG	2384	
Db	1486	CCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGTAACTCACAATTAATG	1545	
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 Qy 2505 CTGACTCGCTCGCTCGGTCGTTTCGGCTGGCGGAGCGGATCAGCTCACTCAAGAGCGG 2564
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 Qy 2565 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTGAGCAAAAGGCC 2624
 Db 1726 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTGAGCAAAAGGCC 1785
 Qy 2625 AGCAAAAGGCCAGGAAACCGTAAAAAGGCCGCTGCTGGCGGCTTTTCCATAGGCTCCGCC 2684
 Db 1786 AGCAAAAGGCCAGGAAACCGTAAAAAGGCCGCTGCTGGCGGCTTTTCCATAGGCTCCGCC 1845
 Qy 2685 CCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAAGAGTGGCGAAACCCGACAGGAC 2744
 Db 1846 CCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAAGAGTGGCGAAACCCGACAGGAC 1905
 Qy 2745 TATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 2804
 Db 1906 TATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 1965
 Qy 2805 TCGCGCTTACCGGATACCTGTCGGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCTCAAT 2864
 Db 1966 TCGCGCTTACCGGATACCTGTCGGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCTCAAT 2025
 Qy 2865 GCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGCTTCCAGTGGCTGTGTGC 2924
 Db 2026 GCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGCTTCCAGTGGCTGTGTGC 2085
 Qy 2925 ACGAACCCCGGTTTCAGCGCCGACCGCTGCGCTTATCCGGTAACATATCGTCTTGAGTCCA 2984
 Db 2086 ACGAACCCCGGTTTCAGCGCCGACCGCTGCGCTTATCCGGTAACATATCGTCTTGAGTCCA 2145
 Qy 2985 ACCCGGTAAGACACGACTTATCGCACTGGCAGGAGCCACTGGTAACAGGATTAGCAGAG 3044
 Db 2146 ACCCGGTAAGACACGACTTATCGCACTGGCAGGAGCCACTGGTAACAGGATTAGCAGAG 2205
 Qy 3045 CGAGTGTATAGCGGCTGCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGCTACACTA 3104
 Db 2206 CGAGTGTATAGCGGCTGCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGCTACACTA 2265
 Qy 3105 GAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 3164
 Db 2266 GAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 2325
 Qy 3165 GTAGCTCTTGATCCGGCAAAAGAAACCAACCGCTGGTAGCGGTGGTTTTTGTTCGAAGC 3224
 Db 2326 GTAGCTCTTGATCCGGCAAAAGAAACCAACCGCTGGTAGCGGTGGTTTTTGTTCGAAGC 2385
 Qy 3225 AGCAGATTACGGCGCAAGAAAAAGGATCTCAAGAAAGATCTTTGATCTTTTCTACGGGCT 3284
 Db 2386 AGCAGATTACGGCGCAAGAAAAAGGATCTCAAGAAAGATCTTTGATCTTTTCTACGGGCT 2445
 Qy 3285 CTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGATTTTGTGTCATGAGCGGATACATAT 3344
 Db 2446 CTGACGC----- 2452
 Qy 3345 TTGAATGTATTTAGAAAAATAACAAATAGGGGTTCCGGCGACATTTTCCCGAAAGTGC 3404
 Db 2453 ----- 2452
 Qy 3405 CACCTGTATCGGTGTGAATATACCGCACAGATCGGTAGGAGAAATACCGCATCAGGAA 3464
 Db 2453 ----- 2452
 Qy 3465 ATTGTAAAGCTTAATTTACAGAACTCTGCTCAAGAGCGGATAGAGCGGATCGGCTG 3524
 Db 2453 -----TCAGAAAGAACTCGTCAAGAGCGGATAGAGCGGATCGGCTG 2494
 Qy 3525 CGAATCGGAGCGGCGATACCGTAAAGACGAGGAGCGGTACGCCATTTCGCGCGCAAG 3584
 Db 2495 CGAATCGGAGCGGCGATACCGTAAAGACGAGGAGCGGTACGCCATTTCGCGCGCAAG 2554

Qy 3585 CTCTTACGCAATATACCGGTAGCCAAACGCTATGTCTGTATAGCGTTCGCCACACCCAG 3644
 Db 2555 CTCTTACGCAATATACCGGTAGCCAAACGCTATGTCTGTATAGCGTTCGCCACACCCAG 2614
 Qy 3645 CCGGCCACAGTGTGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 3704
 Db 2615 CCGGCCACAGTGTGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 2674
 Qy 3705 GGCAATCCCATGGGTACAGACGAGATCCTCGCGTTCGGGCATGTCTGCCCTTGAGCCCTGGC 3764
 Db 2675 GGCAATCCCATGGGTACAGACGAGATCCTCGCGTTCGGGCATGTCTGCCCTTGAGCCCTGGC 2734
 Qy 3765 GAACAGTTCGGTTCGGCGGAGCCCTGTATGCTCTTCCTCAGATCATCTCTGATCGAAG 3824
 Db 2735 GAACAGTTCGGTTCGGCGGAGCCCTGTATGCTCTTCCTCAGATCATCTCTGATCGAAG 2794
 Qy 3825 ACCGGCTTCATCCGAGTACGTGCTCGCTCGATCGATGTTTCGCTTGGTGTGAAATGG 3884
 Db 2795 ACCGGCTTCATCCGAGTACGTGCTCGCTCGATCGATGTTTCGCTTGGTGTGAAATGG 2854
 Qy 3885 GCAGGTAGCCGGATCAAGCGGTATGCAGCCCGCATTTGCATCAGCCATGATGATACCTTT 3944
 Db 2855 GCAGGTAGCCGGATCAAGCGGTATGCAGCCCGCATTTGCATCAGCCATGATGATACCTTT 2914
 Qy 3945 CTCGGCAGGACAAAGGTGAGATGACAGAGATCTCTGCCCGGACATTCGCCCAATAGCAG 4004
 Db 2915 CTCGGCAGGACAAAGGTGAGATGACAGAGATCTCTGCCCGGACATTCGCCCAATAGCAG 2974
 Qy 4005 CCAGTCTCTTCCCGCTTCAGTGACAAAGTGCAGACAGCTGCGCAAGCAAGCCCGCTCGT 4064
 Db 2975 CCAGTCTCTTCCCGCTTCAGTGACAAAGTGCAGACAGCTGCGCAAGCAAGCCCGCTCGT 3034
 Qy 4065 GGCCAGCCACATAGCCCGCTGCTCTCTTTCAGTTCATTTCAGGGCACCGGACAGTTC 4124
 Db 3035 GGCCAGCCACATAGCCCGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3094
 Qy 4125 GGTCTTGACAAAAAGAACCCGGCGCCCTGCGCTGACGCCGGAACACGGCGGCATCAGA 4184
 Db 3095 GGTCTTGACAAAAAGAACCCGGCGCCCTGCGCTGACGCCGGAACACGGCGGCATCAGA 3154
 Qy 4185 GCAGCGGATTCCTGTTGTGCTCCAGTATAGCAGTAAGCTCTCCACCCAGCGCGCGG 4244
 Db 3155 GCAGCGGATTCCTGTTGTGCTCCAGTATAGCAGTAAGCTCTCCACCCAGCGCGCGG 3214
 Qy 4245 AGAACCCTCGTGCATTCATCTTGTCAATCATGCAAAACGATCTCTCATCTCTCTCTG 4304
 Db 3215 AGAACCCTCGTGCATTCATCTTGTCAATCATGCAAAACGATCTCTCATCTCTCTCTG 3274
 Qy 4305 ATCAGAGCTTCATCCCTGCGGCATCAG 4332
 Db 3275 ATCAGAGCTTCATCCCTGCGGCATCAG 3302

RESULT 2

; US-10-764-818A-12
 ; Sequence 12, Application US/10764818A
 ; Publication No. US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI
 ; TITLE OF INVENTION: HERD ANIMALS
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence for the TI-GHRH plasmid.

US-10-764-818A-12

Query Match 39.7%; Score 1718.4; DB 7; Length 3534;
 Best Local Similarity 90.5%; Pred. No. 7.5e-235;
 Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

Qy	2205	GCACAGCTCAGCTTTTGTTCCTTTAGTGAGGTTAAATTCGAGCTTGGCGTAATCAT	2264
Db	1366	GGCCCGGTACAGCTTTTGTTCCTTTAGTGAGGTTAAATTCGAGCTTGGCGTAATCAT	1425
Qy	2265	GGTCATAGCTGTTTCCTGCTGAAATTTATCGCTCAATTCACAAATACGAG	2324
Db	1426	GGTCATAGCTGTTTCCTGCTGAAATTTATCGCTCAATTCACAAATACGAG	1485
Qy	2325	CCGGAAGCATAAAGTGTAAAGCTTGGGCTGCTAAATGAGTGAGCTAACTCACATTAATTG	2384
Db	1486	CCGGAAGCATAAAGTGTAAAGCTTGGGCTGCTAAATGAGTGAGCTAACTCACATTAATTG	1545
Qy	2385	GGTTGCGCTCACTGCGCTTTTCAGTGGGAAACCTGTGTCGAGCTGCATTAATGAA	2444
Db	1546	GGTTGCGCTCACTGCGCTTTTCAGTGGGAAACCTGTGTCGAGCTGCATTAATGAA	1605
Qy	2445	TCGSCCAACCGCGGGAGAGCGGTTTGGTATTTGGGCGCTTTCGCTTCTCGCTCA	2504
Db	1606	TCGSCCAACCGCGGGAGAGCGGTTTGGTATTTGGGCGCTTTCGCTTCTCGCTCA	1665
Qy	2505	CTGACTGCGCTGCGCTCGGCTGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGG	2564
Db	1666	CTGACTGCGCTGCGCTCGGCTGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGG	1725
Qy	2565	TAATACGGTTATCCACAGATTCAGGGGATAACCGAGGAAAGAACATGTGAGCAAAAGGCC	2624
Db	1726	TAATACGGTTATCCACAGATTCAGGGGATAACCGAGGAAAGAACATGTGAGCAAAAGGCC	1785
Qy	2625	AGCAAAAGGCCAGGAAACCGTAAAGAGCGCGGTGCTGGCGTTTTCATAGCTCGGC	2684
Db	1786	AGCAAAAGGCCAGGAAACCGTAAAGAGCGCGGTGCTGGCGTTTTCATAGCTCGGC	1845
Qy	2685	CCCTGACGAGCATCAAAAATCGACGCTCAAGTTCAGAGGTGGCGAAACCCGACAGGAC	2744
Db	1846	CCCTGACGAGCATCAAAAATCGACGCTCAAGTTCAGAGGTGGCGAAACCCGACAGGAC	1905
Qy	2745	TATAAGATACAGGGCTTTCCCTCGGAAAGCTCCCTGCTGCGCTCTCTGTTTCCGACCC	2804
Db	1906	TATAAGATACAGGGCTTTCCCTCGGAAAGCTCCCTGCTGCGCTCTCTGTTTCCGACCC	1965
Qy	2805	TGCGCGTTACCGGATACCTGCTGCGCTTTCTCCCTTGGGAAAGCGGTTCCTCAAT	2864
Db	1966	TGCGCGTTACCGGATACCTGCTGCGCTTTCTCCCTTGGGAAAGCGGTTCCTCAAT	2025
Qy	2865	GCTCAGCTGTAGGTATCTCAGTTTCGCTGTAGGTGCTTCCCTCAAGCTGGGCTGTGTC	2924
Db	2026	GCTCAGCTGTAGGTATCTCAGTTTCGCTGTAGGTGCTTCCCTCAAGCTGGGCTGTGTC	2085
Qy	2925	ACGAAACCCCGTTACGCGCGACCGGTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCA	2984
Db	2086	ACGAAACCCCGTTACGCGCGACCGGTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCA	2145
Qy	2985	ACCCGGTACAGACGACTTATCGCCACTGCGACGCGCTGCTTAACAGATTAAGAGAG	3044
Db	2146	ACCCGGTACAGACGACTTATCGCCACTGCGACGCGCTGCTTAACAGATTAAGAGAG	2205
Qy	3045	CGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTA	3104
Db	2206	CGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTA	2265
Qy	3105	GAAGGACAGTATTTGATATCGGCTGCTGCTGAAGCGAGTTACTCTTCGGAAGAGTTG	3164
Db	2266	GAAGGACAGTATTTGATATCGGCTGCTGCTGAAGCGAGTTACTCTTCGGAAGAGTTG	2325
Qy	3165	GTAGCTCTTGATCCGCAACAAACACCGCTGCTGAGCGGTGTTTTTTTGTTCGAGC	3224
Db	2326	GTAGCTCTTGATCCGCAACAAACACCGCTGCTGAGCGGTGTTTTTTTGTTCGAGC	2385

Qy	3225	AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGT	3284
Db	2386	AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGT	2445
Qy	3285	CTGACGCTCAGTGGAAACGAAACTCACTGTTAAGGATTTTGGTCATGAGCGGATACATAT	3344
Db	2446	CTGACGCTCAGTGGAAACGAAACTCACTGTTAAGGATTTTGGTCATGAGCGGATACATAT	3404
Qy	3345	TTGAATGTATTATAGAAAAATAAACAATAGGGGTTTCGGCGCACATTTCCCGGAAAGTGC	3404
Db	2453	TTGAATGTATTATAGAAAAATAAACAATAGGGGTTTCGGCGCACATTTCCCGGAAAGTGC	2452
Qy	3405	CACCTGTATGCGGTGTAATAATACCGCACAGATCGCTAAGGAGAAATACCGCATCAGGAA	3464
Db	2453	CACCTGTATGCGGTGTAATAATACCGCACAGATCGCTAAGGAGAAATACCGCATCAGGAA	2452
Qy	3465	ATTGTAAGCTTAAATTAATTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTG	3524
Db	2453	ATTGTAAGCTTAAATTAATTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTG	2494
Qy	3525	CGAATCGGAGCGGCGATACCGTAAAGCAGAGGAAGCGGTCAAGCCATTTCCGCGCCCAAG	3584
Db	2495	CGAATCGGAGCGGCGATACCGTAAAGCAGAGGAAGCGGTCAAGCCATTTCCGCGCCCAAG	2554
Qy	3585	CTCTTCAGCAATATACCGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG	3644
Db	2555	CTCTTCAGCAATATACCGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG	2614
Qy	3645	CGCGCCACAGTTCGATGAATCCAGAAAGCGGCAATTTTCCACATGATATTCGGCAAGCA	3704
Db	2615	CGCGCCACAGTTCGATGAATCCAGAAAGCGGCAATTTTCCACATGATATTCGGCAAGCA	2674
Qy	3705	GGCATCGCATGGGTCAAGCAGGATCTTCGCGGTGGGCGATGCTCGCTTGGAGCTGGC	3764
Db	2675	GGCATCGCATGGGTCAAGCAGGATCTTCGCGGTGGGCGATGCTCGCTTGGAGCTGGC	2734
Qy	3765	GAACAGTTCGGGTGGCGCGAGCCCTGATGCTCTTCGTCCAGATCATCTCTGATCGACAAG	3824
Db	2735	GAACAGTTCGGGTGGCGCGAGCCCTGATGCTCTTCGTCCAGATCATCTCTGATCGACAAG	2794
Qy	3825	ACCGGCTTCATCCGAGTACGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGATGG	3884
Db	2795	ACCGGCTTCATCCGAGTACGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGATGG	2854
Qy	3885	GCAGGTAGCGGATCAAGCGTATGAGCGCGCATTCGATCAGCCATGATGATGATCTTT	3944
Db	2855	GCAGGTAGCGGATCAAGCGTATGAGCGCGCATTCGATCAGCCATGATGATGATCTTT	2914
Qy	3945	CTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAG	4004
Db	2915	CTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAG	2974
Qy	4005	CCAGTCCCTTCCCGTTTCACTGACAAACGTCGAGACAGCTGCGCAAGAAACGCGCGTCTG	4064
Db	2975	CCAGTCCCTTCCCGTTTCACTGACAAACGTCGAGACAGCTGCGCAAGAAACGCGCGTCTG	3034
Qy	4065	GGCCAGCAGATAGCGCGCTGCTGCTTTCAGTTCAGGTCAGGTCAGGTCAGGTCAGGTC	4124
Db	3035	GGCCAGCAGATAGCGCGCTGCTGCTTTCAGTTCAGGTCAGGTCAGGTCAGGTCAGGTC	3094
Qy	4125	GGTCTTTCAGAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGCGCATCAGA	4184
Db	3095	GGTCTTTCAGAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGCGCATCAGA	3154
Qy	4185	GCAGCGGATGCTGTTGTCGCGAGTATAGCGGAATAGCTCTTCCACCAAGCGCGCGG	4244
Db	3155	GCAGCGGATGCTGTTGTCGCGAGTATAGCGGAATAGCTCTTCCACCAAGCGCGCGG	3214
Qy	4245	AGAACTGCTGCTCAATCTTGTTCATCATGCGAAACGATCTTCCTCTCTCTCTG	4304
Db	3215	AGAACTGCTGCTCAATCTTGTTCATCATGCGAAACGATCTTCCTCTCTCTCTG	3274

QY 4305 ATCAGAGCTTGATCCCTCGCCATCAG 4332
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 Db 3275 ATCAGATCTTGTATCCCTCGCCATCAG 3302
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RESULT 3
 US-10-764-818A-13
 ; Sequence 13, Application US/10764818A
 ; Publication No. US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
 ; TITLE OF INVENTION: HERD ANIMALS
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleic acid sequence for the TV-GHRH plasmid.
 US-10-764-818A-13

Query Match 39, 7%; Score 1718.4; DB 7; Length 3534;
 Best Local Similarity 90.5%; Pred. No. 7.5e-235;
 Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

QY 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTAGAGGTTAAATTCAGAGCTTGCGTAATCAT 2264
 Db 1366 GGCCCGGTACCAGCTTTTGTTCCTTTAGTAGAGGTTAAATTCAGAGCTTGCGTAATCAT 1425
 QY 2265 GGTATAGCTGTTCTGTGTGAATTTGTTATCGCTCACAATTCACACACATACGAG 2324
 Db 1426 GGTATAGCTGTTCTGTGTGAATTTGTTATCGCTCACAATTCACACACATACGAG 1485
 QY 2325 CCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTCACATTAAATTG 2384
 Db 1486 CCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTCACATTAAATTG 1545
 QY 2385 GTTTCGCTCACTGCGCCCTTTCCAGTCGGGAAACCTGTGTCGAGCTGCAATTAAGAA 2444
 Db 1546 GTTTCGCTCACTGCGCCCTTTCCAGTCGGGAAACCTGTGTCGAGCTGCAATTAAGAA 1605
 QY 2445 TCGGCCAACGCGCGGGAGAGCGTTTTCGTTATGGCGCTCTTCGCTCTTCCTCGCTCA 2504
 Db 1606 TCGGCCAACGCGCGGGAGAGCGTTTTCGTTATGGCGCTCTTCGCTCTTCCTCGCTCA 1665
 QY 2505 CTGACTCTGCTGCGCTCGGTTCGGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGG 2564
 Db 1666 CTGACTCTGCTGCGCTCGGTTCGGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGG 1725
 QY 2565 TAATACGGTTATCCACAGAAATCAGGGGTAACGAGGAAAGAAACATGTGAGCAAAAGGCC 2624
 Db 1726 TAATACGGTTATCCACAGAAATCAGGGGTAACGAGGAAAGAAACATGTGAGCAAAAGGCC 1785
 QY 2625 AGCAAAAGGCCAGGAAACCGTAAAGAGCGCGCTTCCTGCGCGTTTTTCCATAGGCTCCGCC 2684
 Db 1786 AGCAAAAGGCCAGGAAACCGTAAAGAGCGCGCTTCCTGCGCGTTTTTCCATAGGCTCCGCC 1845
 QY 2685 CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTTCAGAGTGGGGAACCCGACAGGAC 2744
 Db 1846 CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTTCAGAGTGGGGAACCCGACAGGAC 1905
 QY 2745 TATAAGATACACAGCGTTTTCCTCGTGAAGCTCCCTCTGTCGCTCTCTCTGTTCCGACCC 2804
 Db 1906 TATAAGATACACAGCGTTTTCCTCTGGAAGCTCCCTCTGTCGCTCTCTCTGTTCCGACCC 1965
 QY 2805 TCCCGCTTACCAGATACCTGTCCGCGTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTCAAT 2864
 Db 1966 TCCCGCTTACCAGATACCTGTCCGCGTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTCAAT 2025

QY 3945 CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGCACCTTCGCCCAATAGCAG 4004
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Db 2915 CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGCACCTTCGCCCAATAGCAG 2974
| | | | |
QY 4005 CCAGTCCCTTCCCGCTTCAGTGACAACTGAGCAGACAGCTGCGCAAGGAAAGCGCCGTCGT 4064
| | | | |
Db 2975 CCAGTCCCTTCCCGCTTCAGTGACAACTGAGCAGACAGCTGCGCAAGGAAAGCGCCGTCGT 3034
| | | | |
QY 4065 GGCAGCAGCAGATAGCCGCTGCTCTGCTTCTGAGTTCAATCAGGCGCACCGGACAGGTC 4124
| | | | |
Db 3035 GGCAGCAGCAGATAGCCGCTGCTCTGCTGAGTTCAATCAGGCGCACCGGACAGGTC 3094
| | | | |
QY 4125 GGTCTTGACAAAAGAAACCGGGCCCTCGCTGACAGCGGAAACAGCGCGGCATCAGA 4184
| | | | |
Db 3095 GGTCTTGACAAAAGAAACCGGGCCCTCGCTGACAGCGGAAACAGCGCGGCATCAGA 3154
| | | | |
QY 4185 GCAGCCGATGTCGTTGTCGCCAGTCATAGCCGAATAGCTCTCCACCCAAAGGGCGCG 4244
| | | | |
Db 3155 GCAGCCGATGTCGTTGTCGCCAGTCATAGCCGAATAGCTCTCCACCCAAAGGGCGCG 3214
| | | | |
QY 4245 AGAACCTGCGTCAATCATCTTGTTCATCATGCGAAACGATCCTCATCTGTCCTTG 4304
| | | | |
Db 3215 AGAACCTGCGTCAATCATCTTGTTCATCATGCGAAACGATCCTCATCTGTCCTTG 3274
| | | | |
QY 4305 ATCAGAGCTGATCCCTGCGCCATCAG 4332
| | | | |
Db 3275 ATCAGATCTTGATCCCTGCGCCATCAG 3302
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RESULT 4

US-10-764-818A-14
; Sequence 14, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; TITLE OF INVENTION: HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the 15/27/28 GHRH plasmid.
US-10-764-818A-14

Query Match 39.7%; Score 1718.4; DB 7; Length 3534;
Best Local Similarity 90.5%; Pred. No. 7.5e-235;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;
QY 2205 GCCACAGCTCCAGTTTGTTCCTTTAGTGAGGTTAAATTCGAGCTTGCGGTAATCAT 2264
| | | | |
Db 1366 GGCCCGGTACCAGCTTTGTTCCTTTAGTGAGGTTAAATTCGAGCTTGCGGTAATCAT 1425
| | | | |
QY 2265 GGTTCATAGCTGTTCCGTGTGAAATGTTATCGCTCACAATTCACACAAATACGAG 2324
| | | | |
Db 1426 GGTTCATAGCTGTTCCGTGTGAAATGTTATCGCTCACAATTCACACAAATACGAG 1485
| | | | |
QY 2325 CCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTG 2384
| | | | |
Db 1486 CCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTG 1545
| | | | |
QY 2385 CGTTGGCTCAGTCGCGCTTTTCAGTCGGGAAACCTGTCGTCGAGCTGCATTAATGAA 2444
| | | | |
Db 1546 CGTTGGCTCAGTCGCGCTTTTCAGTCGGGAAACCTGTCGTCGAGCTGCATTAATGAA 1605
| | | | |
QY 2445 TCGGCCAAACCGCGGGAGAGCGGTTTGGTATGCGGCTTTCGCTTCTCGCTCA 2504
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Db 1606 TCGGCCAAACCGCGGGAGAGCGGTTTGGTATGCGGCTTTCGCTTCTCGCTCA 1665
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3585 CTCTTACGCAATATCAAGGGTAGCAACGGCTATGTCCTGATAGCGGTCCGCCACCCAG 3644
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Query Match 39.7%; Score 1718.4; DB 7; Length 3534;
Best Local Similarity 90.5%; Pred. No. 7.5e-235;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

QY 2205 GCACAGCTCCAGCTTTTGGTTTCCCTTTAGTAGAGGGTTAAATTTTCGAGCTTCGCGTAATCAT 2264
DB 1366 GGCCCGGTACAGCTTTTGTTCCTTTAGTAGAGGGTTAAATTTTCGAGCTTCGCGTAATCAT 1425
QY 2265 GGTTCATAGCTGTTTCTTCGTGTGAAATTTTATCCGCTCACAATTTCCACACAATACGAG 2324
DB 1426 GGTTCATAGCTGTTTCTTCGTGTGAAATTTTATCCGCTCACAATTTCCACACAATACGAG 1485
QY 2325 CCGGAACATAAAGTGTAAAGCTTGGGGTGCCTTAATGAGTGAGCTAATCATTAATTTG 2384
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QY 2385 CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAACCTGTGTCGACGCTGCATTAATGAA 2444
DB 1546 CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAACCTGTGTCGACGCTGCATTAATGAA 1605
QY 2445 TCGGCCAACCGCGCGGGGAGAGCGGTTTGGGTATTGGGCGCTCTTCCGCTTCTCGCTCA 2504
DB 1606 TCGGCCAACCGCGCGGGGAGAGCGGTTTGGGTATTGGGCGCTCTTCCGCTTCTCGCTCA 1665
QY 2505 CTGACTCGCTCGCTCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGG 2564
DB 1666 CTGACTCGCTCGCTCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGG 1725
QY 2565 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGAGGACAAAAGGCC 2624
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QY 2625 AGCAAAAGGCCAGGAAACCGTAAAAAGGCCGCTTTCGTCGCTTTTTCATAGGCTTCGCGC 2684
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QY 2925 ACRAACCCCGCTTCAGCCCGACCGCTTCGCTTATCCGCTTATCCGCTTCTGAGTCA 2984
DB 2086 ACRAACCCCGCTTCAGCCCGACCGCTTCGCTTATCCGCTTATCCGCTTCTGAGTCA 2145
QY 2985 ACCCGGTAAAGACACGACTTATCGCCATGCGACGACCACTGTAACAGGATTCAGAG 3044
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DB 2266 GAAGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTG 2325
QY 3165 GTAGCTCTTGATCCGCGAAACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTTCGAGC 3224
DB 2326 GTAGCTCTTGATCCGCGAAACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTTCGAGC 2385

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RESULT 5

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US-10-764-818A-15
; Sequence 15, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent; version 3.1
; SEQ ID NO 15
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid sequence for wildtype GHRH.
US-10-764-818A-15

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QY 3225 AGCAGATTAGCGCGAGAAAAAGGATCTCAAGAAGATCCTTGATCTTTTCTACGGGGT 3284
 DB 2386 AGCAGATTAGCGCGAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGGT 2445
 QY 3285 CTGACGCTCAGTGAACGAACCTCAGTTAAGGATTTTGGTCATGAGCGGATACATAT 3344
 DB 2446 CTGACGC----- 2452
 QY 3345 TTGAATGTATTAGAAAAATAAACAAATAGGGTTCCGCGCACATTTCCCGGAAAGTGC 3404
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 DB 2453 -----TCAAGAAACTCGTCAAGAGCGGATAGAGCGGATGCGCTG 2494
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 DB 2615 CCGGCCACAGTCGATGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 2674
 QY 3705 GGCATCGCCATGGGTACAGACAGATCTCTCGCGTCCGGCATGCTCGCTTGGAGCTGGC 3764
 DB 2675 GGCATCGCCATGGGTACAGACAGATCTCTCGCGTCCGGCATGCTCGCTTGGAGCTGGC 2734
 QY 3765 GAACAGTTCCGCTGGCGGAGCCCTGATGCTCTTGTTCAGATCATCTCTGATCGCAAG 3824
 DB 2735 GAACAGTTCCGCTGGCGGAGCCCTGATGCTCTTGTTCAGATCATCTCTGATCGCAAG 2794
 QY 3825 ACCGGCTTCATCCGAGTAGCTGCTCGATCGATGTTTCTGCTTGGTGGTTCGATGG 3884
 DB 2795 ACCGGCTTCATCCGAGTAGCTGCTCGATCGATGTTTCTGCTTGGTGGTTCGATGG 2854
 QY 3885 GCAGGTAGCCGATCAAGCGTATGACAGCGCCGCTGATGATGATGATGATGATGATGAT 3944
 DB 2855 GCAGGTAGCCGATCAAGCGTATGACAGCGCCGCTGATGATGATGATGATGATGATGAT 2914
 QY 3945 CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTGCCCCGCACTTCCGCCCAATAGCAG 4004
 DB 2915 CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTGCCCCGCACTTCCGCCCAATAGCAG 2974
 QY 4005 CAGTCCCTTCCGCTTCAGTGACAGGTGACGACAGCTGCGCAAGGACGCGCTCGT 4064
 DB 2975 CAGTCCCTTCCGCTTCAGTGACAGGTGACGACAGCTGCGCAAGGACGCGCTCGT 3034
 QY 4065 GGCAGCAGCAGATAGCGCGCTGCTGCTTTCAGTTCATTCAGGCGCACCGGACAGGTC 4124
 DB 3035 GGCAGCAGCAGATAGCGCGCTGCTGCTTTCAGTTCATTCAGGCGCACCGGACAGGTC 3094
 QY 4125 GGTCTTGAACAAAGAACCGGGCGCTGCTGCTGATGACGCGGAAACAGCGCGGATCAGA 4184
 DB 3095 GGTCTTGAACAAAGAACCGGGCGCTGCTGCTGATGACGCGGAAACAGCGCGGATCAGA 3154
 QY 4185 GCAGCGGATGCTGTTGTGCCCCAGTCATAGCGAATAGCTCTCCACCCCAAGCGCGG 4244
 DB 3155 GCAGCGGATGCTGTTGTGCCCCAGTCATAGCGAATAGCTCTCCACCCCAAGCGCGG 3214
 QY 4245 AGAACCTGCGTGAATCATCTTTGTTCAATCATCGGAAACGATCTCATCTCTCTCTTG 4304
 DB 3215 AGAACCTGCGTGAATCATCTTTGTTCAATCATCGGAAACGATCTCATCTCTCTCTTG 3274
 QY 4305 ATCAGAGCTTGATCCCTTCGCCCATCAG 4332

DB 3275 ATCAGATCTTGATCCCTCGCCATCAG 3302
 RESULT 6
 US-10-764-818A-29
 ; Sequence 29, Application US/10764818A
 ; Publication No. US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CU
 ; TITLE OF INVENTION: HERD ANIMALS
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10/764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Codon optimized plasmid for GHRH expression.
 US-10-764-818A-29
 Query Match 39.7%; Score 1718.4; DB 7; Length 3534;
 Best Local Similarity 90.5%; Pred. No. 7.5e-235;
 Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;
 QY 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCAGAGCTTGGCGTAATCAT 2264
 DB 1366 GGCCCGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCAGAGCTTGGCGTAATCAT 1425
 QY 2265 GGTATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTTCCACAAATACAGAG 2324
 DB 1426 GGTATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTTCCACAAATACAGAG 1485
 QY 2325 CCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTG 2384
 DB 1486 CCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTG 1545
 QY 2385 CGTTGCGCTCACTGCGCGCTTCCAGTCGCGAAACCTGTCGTCGAGCTGATTAATGAA 2444
 DB 1546 CGTTGCGCTCACTGCGCGCTTCCAGTCGCGAAACCTGTCGTCGAGCTGATTAATGAA 1605
 QY 2445 TCGGCCAACGCGCGGAGAGCGGTTTCGCTATTTGGGCGCTTTCGCTTCTCGCTCA 2504
 DB 1606 TCGGCCAACGCGCGGAGAGCGGTTTCGCTATTTGGGCGCTTTCGCTTCTCGCTCA 1665
 QY 2505 CTGACTCGCTGCGCTCGCTCGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 2564
 DB 1666 CTGACTCGCTGCGCTCGCTCGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 1725
 QY 2565 TAATAGCGTTATCCACAGAAATCAGGGGATTAACGAGAAAGAAACATGTGAGCAAAAGGCC 2624
 DB 1726 TAATAGCGTTATCCACAGAAATCAGGGGATTAACGAGAAAGAAACATGTGAGCAAAAGGCC 1785
 QY 2625 AGCAAAAGCGCAGGAAACCGTAAAGCGCGCTTTCGCTGCTGCTTTTCCATAGGCTCGCC 2684
 DB 1786 AGCAAAAGCGCAGGAAACCGTAAAGCGCGCTTTCGCTGCTGCTTTTCCATAGGCTCGCC 1845
 QY 2685 CCCCTGACGAGCATCAAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 2744
 DB 1846 CCCCTGACGAGCATCAAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 1905
 QY 2745 TATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 2804
 DB 1906 TATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 1965
 QY 2805 TCGCGCTTACCGGATACCTGTCGCGCTTTCCTCTCGGAAAGCGTGGCGCTTCTCAAT 2864
 DB 1966 TCGCGCTTACCGGATACCTGTCGCGCTTTCCTCTCGGAAAGCGTGGCGCTTCTCAAT 2025

Best Local Similarity 90.5%; Pred. No. 7.4e-235;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

QY 2205 GCCACAGCTCCAGGCTTTGTTCCCTTTAGTGAAGGTTAAATTCGAGCTTGGCGTAATCAT 2264
| | | | |
Db 2834 GGCCGGTACCAGCTTTGTTCCCTTTAGTGAAGGTTAAATTCGAGCTTGGCGTAATCAT 2893
| | | | |
QY 2265 GGTATAGCTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAATACGAG 2324
| | | | |
Db 2894 GGTATAGCTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAATACGAG 2953
| | | | |
QY 2325 CCGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGCTTAATCAATTAATTG 2384
| | | | |
Db 2954 GGTATAGCTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAATACGAG 3013
| | | | |
QY 2385 GGTATAGCTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAATACGAG 2444
| | | | |
Db 3014 GGTATAGCTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAATACGAG 3073
| | | | |
QY 2445 TCGGCAACGGCGGGGAGAGCGGTTTGCGTATTTGGGCGCTCTTCCGCTTCTCGCTCA 2504
| | | | |
Db 3074 TCGGCAACGGCGGGGAGAGCGGTTTGCGTATTTGGGCGCTCTTCCGCTTCTCGCTCA 3133
| | | | |
QY 2505 CTGACTCGCTCGGCTCGGCTCGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGG 2564
| | | | |
Db 3134 CTGACTCGCTCGGCTCGGCTCGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGG 3193
| | | | |
QY 2565 TAATACGGTTATCCACAGATCAGGGGATACGAGGAAAGAAACATGTGAGCAAAAGGCC 2624
| | | | |
Db 3194 TAATACGGTTATCCACAGATCAGGGGATACGAGGAAAGAAACATGTGAGCAAAAGGCC 3253
| | | | |
QY 2625 AGCAAAAGCCAGGAAACCGTAAAGGCGGTTGCTGGCGTTTTCATAGGCTCGCC 2684
| | | | |
Db 3254 AGCAAAAGCCAGGAAACCGTAAAGGCGGTTGCTGGCGTTTTCATAGGCTCGCC 3313
| | | | |
QY 2685 CCCCTGAGAGCATCACAAGATCAGCTCAAGTCAGAGTGGCGAAGCCGACAGGAC 2744
| | | | |
Db 3314 CCCCTGAGAGCATCACAAGATCAGCTCAAGTCAGAGTGGCGAAGCCGACAGGAC 3373
| | | | |
QY 2745 TATAAGATACAGGCGTTTCCCTCGGAGCTCCCTGCGGCTCTCTGTTCCGACCC 2804
| | | | |
Db 3374 TATAAGATACAGGCGTTTCCCTCGGAGCTCCCTGCGGCTCTCTGTTCCGACCC 3433
| | | | |
QY 2805 TCCCGTTACCGGATACCTGTCGCGCTTTCCTCTCGGAAAGCGTGGCTTCTCAAT 2864
| | | | |
Db 3434 TCCCGTTACCGGATACCTGTCGCGCTTTCCTCTCGGAAAGCGTGGCGCTTCTCAT 3493
| | | | |
QY 2865 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTCTGCTCCAGCTGGGCTGTGTGC 2924
| | | | |
Db 3494 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTCTGCTCCAGCTGGGCTGTGTGC 3553
| | | | |
QY 2925 ACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCA 2984
| | | | |
Db 3554 ACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCA 3613
| | | | |
QY 2985 ACCCGTTAAGACAGACTTATCCGACCTGGCAGCAGCAGCTGGTAAACAGGATAGCAG 3044
| | | | |
Db 3614 ACCCGTTAAGACAGACTTATCCGACCTGGCAGCAGCAGCTGGTAAACAGGATAGCAG 3673
| | | | |
QY 3045 CAGGTTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACACGGCTACACTA 3104
| | | | |
Db 3674 CAGGTTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACACGGCTACACTA 3164
| | | | |
QY 3105 GAAGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTACCTTCGGAAGAGTTG 3164
| | | | |
Db 3734 GAAGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTG 3793
| | | | |
QY 3165 GTAGCTCTTGTATCCGCAACAAACCAACCGCTGGTAGCGGTGTTTTTGTGTTGCAAGC 3224
| | | | |
Db 3794 GTAGCTCTTGTATCCGCAACAAACCAACCGCTGGTAGCGGTGTTTTTGTGTTGCAAGC 3853
| | | | |
QY 3225 AGCAGATTACGGCGCAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTCTTACGGGCT 3284
| | | | |

Db 3854 AGCAGATTACGGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGT 3913
| | | | |
QY 3285 CTGACGCTCAGTGGAAACGAAACCTCACTTTAAGGATTTTGGTCATGAGCGGATACATAT 3344
| | | | |
Db 3914 CTGACGCTTTTGAAGGATTTTGGTCATGAGCGGATACATAT 3920
| | | | |
QY 3345 TTGAATGTATTAGAAAAATAAACAATAGGGTTCCGCGCACATTTCCCGGAAAAAGTGC 3404
| | | | |
Db 3921 ----- 3920
| | | | |
QY 3405 CACCTGTATGGGTGTGAATATCCGACAGATGCGTAAAGGAAAAATACCGCATCAGGAA 3464
| | | | |
Db 3921 ----- 3920
| | | | |
QY 3465 ATTGTAAAGGTTAATAATTTCAGAAAGAACTCTCAAGAAAGGCGATAGAAAGGCGATGCGCTG 3524
| | | | |
Db 3921 -----TCAGAAAGAACTCTCAAGAAAGGCGATAGAAAGGCGATGCGCTG 3962
| | | | |
QY 3525 CGAATCGGAGCGCGATACCGTAAAGCAGAGAAAGCGGTCAAGCCATTCGCGCCAAAG 3584
| | | | |
Db 3963 CGAATCGGAGCGCGATACCGTAAAGCAGAGAAAGCGGTCAAGCCATTCGCGCCAAAG 4022
| | | | |
QY 3585 CTCTTCAGCAATATCACGGGTAGCCAAAGCTATGTCTGTATAGCGGTCCGCCACACCCAG 3644
| | | | |
Db 4023 CTCTTCAGCAATATCACGGGTAGCCAAAGCTATGTCTGTATAGCGGTCCGCCACACCCAG 4082
| | | | |
QY 3645 CCGGCCACAGTTCAGTAAATCCAGAAAGCGGCGCATTTTCCACCATGATATTTCGGCAAGCA 3704
| | | | |
Db 4083 CCGGCCACAGTTCAGTAAATCCAGAAAGCGGCGCATTTTCCACCATGATATTTCGGCAAGCA 4142
| | | | |
QY 3705 GGCAATCGCATTTGGTTCAGACAGATCTCCGCTCGGCGATGCTCGCTTTGAGCTTGGC 3764
| | | | |
Db 4143 GGCAATCGCATTTGGTTCAGACAGATCTCCGCTCGGCGATGCTCGCTTTGAGCTTGGC 4202
| | | | |
QY 3765 GAAACAGTTTCGGTTCGCGAGCGCTGATGCTCTTCGTCAGATCATCTTCATGACACAG 3824
| | | | |
Db 4203 GAAACAGTTTCGGTTCGCGAGCGCTGATGCTCTTCGTCAGATCATCTTCATGACACAG 4262
| | | | |
QY 3825 ACCGCTTTCATTCGAGTACGTCGCTCGATGCGATGTTTCGCTTGGTTCGATGCG 3884
| | | | |
Db 4263 ACCGCTTTCATTCGAGTACGTCGCTCGATGCGATGTTTCGCTTGGTTCGATGCG 4322
| | | | |
QY 3885 GCAGTACGCGATCAAGCGTATGACGCGCGCATTCATCAGCCATGATGATGATGATGAT 3944
| | | | |
Db 4323 GCAGTACGCGATCAAGCGTATGACGCGCGCATTCATCAGCCATGATGATGATGATGAT 4382
| | | | |
QY 3945 CTGCGCAGGACGAGGTGAGATGACAGAGATCTTCGCGCGGCACTTCGCGCAATAGCAG 4004
| | | | |
Db 4383 CTGCGCAGGACGAGGTGAGATGACAGAGATCTTCGCGCGGCACTTCGCGCAATAGCAG 4442
| | | | |
QY 4005 CCAGTCCCTTCCGCTTCAGTGACAAAGTCGAGCAGCTGCGAAGGAAACGCGCTGCT 4064
| | | | |
Db 4443 CCAGTCCCTTCCGCTTCAGTGACAAAGTCGAGCAGCTGCGAAGGAAACGCGCTGCT 4502
| | | | |
QY 4065 GSCCAGCAGCATAGCTGCGCTGCTTCGTCAGTTCATTCAGGCGCACCGGACAGGTC 4124
| | | | |
Db 4503 GSCCAGCAGCATAGCTGCGCTGCTTCGTCAGTTCATTCAGGCGCACCGGACAGGTC 4562
| | | | |
QY 4125 GGTCTTGAACAAAGAACCGGCGCGCTTCGCTGACAGCGGAAACACGCGGCGATCAGA 4184
| | | | |
Db 4563 GGTCTTGAACAAAGAACCGGCGCGCTTCGCTGACAGCGGAAACACGCGGCGATCAGA 4622
| | | | |
QY 4185 GCAGCGGATGCTGCTGTCGCGGCGCTTCATAGCGGATAGCTCTCCACCAAGCGGCGG 4244
| | | | |
Db 4623 GCAGCGGATGCTGCTGTCGCGGCGCTTCATAGCGGATAGCTCTCCACCAAGCGGCGG 4682
| | | | |
QY 4245 AGAATCTGCTGCAATTCATCTTGTTCATCATGCGAAACGATCTTCATCTGCTCTCTTG 4304
| | | | |
Db 4683 AGAATCTGCTGCAATTCATCTTGTTCATCATGCGAAACGATCTTCATCTGCTCTCTTG 4742
| | | | |
QY 4305 ATCAGAGCTTGATCCCTTCGCGCATCAG 4332
| | | | |
Db 4743 ATCAGATCTTGATCCCTTCGCGCATCAG 4770
| | | | |

QY 3824 GACCGGCTTCATCCGAGTACGTCTCGTCCGATCGCATGTTTCGCTTGGTGGTCAATG 3883
DB GACCGGCTTCATCCGAGTACGTCTCGTCCGATCGCATGTTTCGCTTGGTGGTCAATG 3803
QY 3884 GCGAGGTAGCGGATCAAGCGTATGTCAGCGCGCGCATTTGCAATGATGATATCTT 3943
DB GCGAGGTAGCGGATCAAGCGTATGTCAGCGCGCGCATTTGCAATGATGATATCTT 3743
QY 3944 TCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTGCGCGGCACTTCGCGCCCAATAGCA 4003
DB TCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTGCGCGGCACTTCGCGCCCAATAGCA 3683
QY 4004 GCGAGTCCCTCCCGCTTCAGTGAACAAGTGCAGACAGTGCAGGAACGCGCGTCG 4063
DB GCGAGTCCCTCCCGCTTCAGTGAACAAGTGCAGACAGTGCAGGAACGCGCGTCG 3623
QY 4064 TGGCCAGCAGCATAGCGCGCTCGCTCGTCTGCGATTCATTCAGGGCAGCGACAGGT 4123
DB TGGCCAGCAGCATAGCGCGCTCGCTCGTCTGCGATTCATTCAGGGCAGCGACAGGT 3563
QY 4124 CGGTCTTGACAAAAGAACCGGCGCGCTCGCTGAGCAGCGGAACAACGGCGGCATCAG 4183
DB CGGTCTTGACAAAAGAACCGGCGCGCTCGCTGAGCAGCGGAACAACGGCGGCATCAG 3503
QY 4184 AGCAGCGATGTCTGTTGTCGCCAGTCATAGCCGAATAGCTCTCCACCCCAAGCGCGC 4243
DB AGCAGCGATGTCTGTTGTCGCCAGTCATAGCCGAATAGCTCTCCACCCCAAGCGCGC 3443
QY 4244 GAGAACCTGCGTGAATCCATCTGTTCAATCATGCGAAGATCTCTCTCTCTCTT 4303
DB GAGAACCTGCGTGAATCCATCTGTTCAATCATGCGAAGATCTCTCTCTCTCTT 3383
QY 4304 GATCAGAGCTTGATCCCTCGGCCATCAG 4332
DB GATCAGAGCTTGATCCCTCGGCCATCAG 3354

RESULT 11

US-11-186-282-23
; Sequence 23, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advlsys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186.282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having a codon optimized mouse GHRH sequence
US-11-186-282-23

Query Match 33.7%; Score 1457.8; DB 12; Length 2722;
Best Local Similarity 88.9%; Pred. No. 5.9e-198;
Matches 1664; Conservative 0; Mismatches 27; Indels 180; Gaps 1;
QY 2462 AGAGCGGTTGGCGTATTTGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTCGCTCG 2521
DB 860 AGTGGAGGTTAAATTCGAGCTTGGCTTCTCGCTTCTCGCTCACTGACTCGCTCGCTCG 919
QY 2522 GTGCTTCGCTCGCGGAGCGGTATCAGTCACTCAAGGCGGTAATACGGTTATCCACA 2581
DB 920 GTGCTTCGCTTCGCGGAGCGGTATCAGTCACTCAAGGCGGTAATACGGTTATCCACA 979
QY 2582 GAATCAGGGATATACGAGGAAAGAACATGTGACAAAAGCCAGCAAAAGGCGCAGGAAC 2641
DB 980 GAATCAGGGATATACGAGGAAAGAACATGTGACAAAAGGCGCAGGAAC 1039

QY 2642 CGTAAAGAGCGCGTGTGCTGGCGTCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC 2701
DB CGTAAAGAGCGCGTGTGCTGGCGTCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC 1099
QY 2702 AAAAATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATATAAGATACAGGCG 2761
DB AAAAATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATATAAGATACAGGCG 1159
QY 2762 TTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC 2821
DB TTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC 1219
QY 2822 CTGTCGCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGATAGTAT 2881
DB CTGTCGCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGATAGTAT 1279
QY 2882 CTGATTCGGTGTAGGTGCTTCGCTCAAGTGGGCTGTGTGACGAAACCCCGCTTCAG 2941
DB CTGATTCGGTGTAGGTGCTTCGCTCAAGTGGGCTGTGTGACGAAACCCCGCTTCAG 1339
QY 2942 CCGACCGCTGCGCTTTATCCGGTAACTATCTGCTTCAAGTGGGCTGTGTGACGAAACCCCGCTTCAG 3001
DB CCGACCGCTGCGCTTTATCCGGTAACTATCTGCTTCAAGTGGGCTGTGTGACGAAACCCCGCTTCAG 1399
QY 3002 TTATCGCCACTGGCAGCAGCCACTGTGTAAACAGGATTTAGCAGAGCGAGGTATGTAGCGGT 3061
DB TTATCGCCACTGGCAGCAGCCACTGTGTAAACAGGATTTAGCAGAGCGAGGTATGTAGCGGT 1459
QY 3062 GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGCTTACACTAGAAAGACAGTATTTGGT 3121
DB GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGCTTACACTAGAAAGACAGTATTTGGT 1519
QY 3122 ATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGGAGTTGCTAGCTCTTTGATCCGGC 3181
DB ATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGGAGTTGCTAGCTCTTTGATCCGGC 1579
QY 3182 AAAACAAACCCGCTGTAGCGGTGTTTTTTTGTTCGAAAGCAGCAGATTTACGCGCAGA 3241
DB AAAACAAACCCGCTGTAGCGGTGTTTTTTTGTTCGAAAGCAGCAGATTTACGCGCAGA 1639
QY 3242 AAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGCTGTGACGCTCAGTGGAC 3301
DB AAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGCTGTGACGCTCAGTGGAC 1693
QY 3302 GAAAACTACGTTAAAGGATTTTGGTTCATGAGCGGATACATATTTGAATGTATTTAGAAA 3361
DB GAAAACTACGTTAAAGGATTTTGGTTCATGAGCGGATACATATTTGAATGTATTTAGAAA 1693
QY 3362 AATAAAATAAGGGTTTCGCGCACATTTTCCCGAAAAGTGCACCTGTATGCGGTGTG 3421
DB AATAAAATAAGGGTTTCGCGCACATTTTCCCGAAAAGTGCACCTGTATGCGGTGTG 1693
QY 3422 AATACCGCACAGTGGTAAAGGAAATAATCCGCATCAGAAATTTGTAAGCGTTAATAA 3481
DB AATACCGCACAGTGGTAAAGGAAATAATCCGCATCAGAAATTTGTAAGCGTTAATAA 1699
QY 3482 TTCAGAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGTGGAAATCGGAGCGCGA 3541
DB TTCAGAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGTGGAAATCGGAGCGCGA 1759
QY 3542 TACCGTAAAGCAGAGGAGCGGTCAAGCCATTTTCGCGCGCAAGCTCTTCAGCAATATCAC 3601
DB TACCGTAAAGCAGAGGAGCGGTCAAGCCATTTTCGCGCGCAAGCTCTTCAGCAATATCAC 1819
QY 3602 GGGTAGCCAACTGTCTCTGATAGCGGTCCGCAACCCAGCCGCGCACAGTCCGATGA 3661
DB GGGTAGCCAACTGTCTCTGATAGCGGTCCGCAACCCAGCCGCGCACAGTCCGATGA 1879
QY 3662 ATCCAGAAAAGCGCGCATTTTCCACCATGATATTTCCGCAAGCAGGATCCCATGGGTCA 3721
DB ATCCAGAAAAGCGCGCATTTTCCACCATGATATTTCCGCAAGCAGGATCCCATGGGTCA 1939
QY 3722 CGACGAGATCTCTCGCGTGGGCAATGCTCGCTTGTAGCCTTGGGCAACAGTTTCGCGTGGCG 3781

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Db      1940  CGACGAGATCTCGCGCTCGGCGATGCGCGCTTTGAGCTGCGGAACAGATTTCGCTGCGC 1999
Qy      3782  CGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAG 3841
Db      2000  CGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAG 2059
Qy      3842  TACGTGCTCGCTCGATGCGATGTTTTCGTTGCTGCTGATGCGAATGGGAGGTAGCCGATCAA 3901
Db      2060  TACGTGCTCGCTCGATGCGATGTTTTCGTTGCTGCTGATGCGAATGGGAGGTAGCCGATCAA 2119
Qy      3902  GCGTATGAGCGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3961
Db      2120  GCGTATGAGCGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2179
Qy      3962  GAGATGACAGAGATCTGCGCGCGCTTCGCGCAATAGCAGCGAGTCCCTTCCCGCTT 4021
Db      2180  GAGATGACAGAGATCTGCGCGCGCTTCGCGCAATAGCAGCGAGTCCCTTCCCGCTT 2239
Qy      4022  CAGTGACAACTGCGAGCAGCTGCGCAAGAAAGCGCGCTGCGCGAGCGCAAGATGATGATGATG 4081
Db      2240  CAGTGACAACTGCGAGCAGCTGCGCAAGAAAGCGCGCTGCGCGAGCGCAAGATGATGATGATG 2299
Qy      4082  GCGTGCCTGCTGCTGCGAGTTCATTCAGGCGACCGGAGCGTCTGTCGACAAAGAA 4141
Db      2300  GCGTGCCTGCTGCTGCGAGTTCATTCAGGCGACCGGAGCGTCTGTCGACAAAGAA 2359
Qy      4142  CCGGCGCGCTGCGCTGACAGCGGAAACAGCGCGGATCAGAGCAGCGGATGCTGCTT 4201
Db      2360  CCGGCGCGCTGCGCTGACAGCGGAAACAGCGCGGATCAGAGCAGCGGATGCTGCTT 2419
Qy      4202  GTGCCAGTCAATAGCGAATAGCTCTCCACCAAGCGCGCGGAACTGCGTCAATC 4261
Db      2420  GTGCCAGTCAATAGCGAATAGCTCTCCACCAAGCGCGCGGAACTGCGTCAATC 2479
Qy      4262  CATCTGTTCAATGCGAAGAGTCTCATCTGCTGCTGATCAGAGTGTGATGATGATGATGATG 4321
Db      2480  CATCTGTTCAATGCGAAGAGTCTCATCTGCTGCTGATCAGAGTGTGATGATGATGATGATG 2539
Qy      4322  TCGCGCATCAG 4332
Db      2540  TCGCGCATCAG 2550

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RESULT 12
US-11-186-282-24
; Sequence 24, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVS1-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 24
; LENGTH: 2725
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having a codon optimized rat GHRH sequence
US-11-186-282-24

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Query Match      33.7%; Score 1457.8; DB 12; Length 2725;
Best Local Similarity 88.9%; Pred. No. 5,9e-198;
Matches 1664; Conservative 0; Mismatches 27; Indels 180; Gaps 1;

Qy      2462  AGAGCGCGTTGGTATGCGGCTCTTCGCTTCTCGTCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 2521
Db      863  AGTGAAGGTTAATTCGAGCTTGGTCTTCGCTTCTCGCTTCTCGTCTACTGACTGCTGCTGCTG 922
Qy      2522  GTCGTTGCGCTGCGGCGGCTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACA 2581

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Db      923  GTCTGTCGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACA 982
Qy      2582  GAATCAGGGGATACGAGGAAAGAAATGATGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 2641
Db      983  GAATCAGGGGATACGAGGAAAGAAATGATGAGCAAAAGGCCAGCAAAAGGCCAGGAAC 1042
Qy      2642  CGTAAAGGCGCGTGTGCGCTTTTTCATAGGCTCCGCCCCCTCGAGCAGCATCAC 2701
Db      1043  CGTAAAGGCGCGTGTGCGCTTTTTCATAGGCTCCGCCCCCTCGAGCAGCATCAC 1102
Qy      2702  AAAAAATCGACGCTCAAGTCAAGAGTGGGAAACCCGACAGGACTATAAAGATACCAAGCG 2761
Db      1103  AAAAAATCGACGCTCAAGTCAAGAGTGGGAAACCCGACAGGACTATAAAGATACCAAGCG 1162
Qy      2762  TTTCCCTCGAAGCTCCCTCGTCCGCTCTCTCTGTCGACCCCTCGCGCTTACCGGATAC 2821
Db      1163  TTTCCCTCGAAGCTCCCTCGTCCGCTCTCTCTGTCGACCCCTCGCGCTTACCGGATAC 1222
Qy      2822  CTGTCGCGCTTCTCCCTTCGCGAAGCGTGGCGCTTCTCAATGCTCAGCGCTAGGTAT 2881
Db      1223  CTGTCGCGCTTCTCCCTTCGCGAAGCGTGGCGCTTCTCAATGCTCAGCGCTAGGTAT 1282
Qy      2882  CTCAAGTTCGCGTGTAGGCTCGCTTCCAAAGCTGGGCTGTGTCAGAAACCCCGCTTCAG 2941
Db      1283  CTCAAGTTCGCGTGTAGGCTCGCTTCCAAAGCTGGGCTGTGTCAGAAACCCCGCTTCAG 1342
Qy      2942  CCGACCGCTCGCGCTTATCCGCTAACTATCGTCTTGTAGTCAACCCCGGTAAAGACAGAC 3001
Db      1343  CCGACCGCTCGCGCTTATCCGCTAACTATCGTCTTGTAGTCAACCCCGGTAAAGACAGAC 1402
Qy      3002  TTATCGCCACTGCGCAGCGACCACTGGTAAACAGGATTAGCAGAGCGAGTATGTAGCGGT 3061
Db      1403  TTATCGCCACTGCGCAGCGACCACTGGTAAACAGGATTAGCAGAGCGAGTATGTAGCGGT 1462
Qy      3062  GCTACAGAGTCTTGAAGTGTGGCTAACTACCGCTACCTAGAAAGACAGTATTTGGT 3121
Db      1463  GCTACAGAGTCTTGAAGTGTGGCTAACTACCGCTACCTAGAAAGACAGTATTTGGT 1522
Qy      3122  ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTGTGTAGTCTTTGATCCGGC 3181
Db      1523  ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTGTGTAGTCTTTGATCCGGC 1582
Qy      3182  AAAAACAACCGCTGCTGAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3241
Db      1583  AAAAACAACCGCTGCTGAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1642
Qy      3242  AAAAAAGGATCTCAAGAAAGATCCTTTGATCTTTTCTAGCGGTCTGACGCTCAGTGGAAAC 3301
Db      1643  AAAAAAGGATCTCAAGAAAGATCCTTTGATCTTTTCTAGCGGTCTGACGCTCAG----- 1696
Qy      3302  GAAAACTCACGTTAAGGATTTTGTGTCATGAGCGGATACATATTTGAATGTATTTAGAAA 3361
Db      1697  ----- 1696
Qy      3362  AATAACAATAAGGGTTCCGCGCACATTTCCCGGAAAGTCCACCTGTATGCGGTGTG 3421
Db      1697  ----- 1696
Qy      3422  AATAACCGCACAGATCGGTAGGAGAAAATACCGCATCAGAAATTTGTAAGCGTTAATAA 3481
Db      1697  -----CTAGCG 1702
Qy      3482  TTCAGAAAGTCTGCTCAAGAGCGGATAGAGCGGATGCGCTCGGATCGGAGCGCGCA 3541
Db      1703  CTCAGAAAGTCTGCTCAAGAGCGGATAGAGCGGATGCGCTCGGATCGGAGCGCGCA 1762
Qy      3542  TACCGTAAAGCAGGAGGAGCGCTCAGCCCATTTCCGCGCAAGCTCTTTCAGCAATATCAC 3601
Db      1763  TACCGTAAAGCAGGAGGAGCGCTCAGCCCATTTCCGCGCAAGCTCTTTCAGCAATATCAC 1822
Qy      3602  GGTAGCCCAACGCTATGCTCTGATAGCGGTCCGCCACAACCCAGCGCGGCAAGTGCATGA 3661

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Db 1823 GGGTAGCCAGCGCTATGTCCTGATAGACGGGTCCGCCACACCCGCCGCCACAGTGATGA 1882
 QY 3662 ATCCAGAAAAGCGCCATTTCCTACCATGATATTTGGCAGAGGAGCATGCGATGGTCA 3721
 Db 1883 ATCCAGAAAAGCGCCATTTCCTACCATGATATTTGGCAGAGGAGCATGCGATGGTCA 1942
 QY 3722 CGACAGATTCCTCGCGGTGGGAGTGTGCGCTTGAAGCTGGCGAAAGTTGGGTGGCG 3781
 Db 1943 CGACAGATTCCTCGCGGTGGGAGTGTGCGCTTGAAGCTGGCGAAAGTTGGGTGGCG 2002
 QY 3782 CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATGCAAGACCGGCTTTCATCCAG 3841
 Db 2003 CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATGCAAGACCGGCTTTCATCCAG 2062
 QY 3842 TACGTGCTGCTCGATGCGATTTTTCGCTTGGTGTGCAATGGGCAAGTACCGATCA 3901
 Db 2063 TACGTGCTGCTCGATGCGATTTTTCGCTTGGTGTGCAATGGGCAAGTACCGATCA 2122
 QY 3902 GCGTATGACGCGCGCATGTCATGATGATGATGATGATGATGATGATGATGATGATG 3961
 Db 2123 GCGTATGACGCGCGCATGTCATGATGATGATGATGATGATGATGATGATGATGATG 2182
 QY 3962 GAGATGACGAGATCTGCGCCCGGCACTTCCGCAATAGCAGCAGTCCCTTCCGCTT 4021
 Db 2183 GAGATGACGAGATCTGCGCCCGGCACTTCCGCAATAGCAGCAGTCCCTTCCGCTT 2242
 QY 4022 CAGTACACAGTTCAGACACAGTGTGCGAGAGAACCCCGTGTGGCCAGCCAGATGCC 4081
 Db 2243 CAGTACACAGTTCAGACACAGTGTGCGAGAGAACCCCGTGTGGCCAGCCAGATGCC 2302
 QY 4082 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4141
 Db 2303 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2362
 QY 4142 CCGGCGCGCCCTGCGCTGACAGCCGGAACACCGCGCGCATCAGAGAGCGCATTTGCTGT 4201
 Db 2363 CCGGCGCGCCCTGCGCTGACAGCCGGAACACCGCGCGCATCAGAGAGCGCATTTGCTGT 2422
 QY 4202 GTGCCCATCATAGCGGAAATAGCTCTTCCACCAAGCGCGCGGAGAACCTGCTGCAATC 4261
 Db 2423 GTGCCCATCATAGCGGAAATAGCTCTTCCACCAAGCGCGCGGAGAACCTGCTGCAATC 2482
 QY 4262 CATCTTGTTCATCATGCGAAACGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4321
 Db 2483 CATCTTGTTCATCATGCGAAACGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2542
 QY 4322 TGCGCCATCAG 4332
 Db 2543 TGCGCCATCAG 2553

RESULT 13
 US-11-186-282-33
 ; Sequence 33, Application US/11186282
 ; Publication No. US20060025368A1

; GENERAL INFORMATION:
 ; APPLICANT: AdviaSys, Inc.

; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
 ; FILE REFERENCE: 108328.000265 AVSI-0042
 ; CURRENT APPLICATION NUMBER: US/11/186,282
 ; CURRENT FILING DATE: 2005-07-21
 ; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 33

; LENGTH: 2700
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: This is the optimized plasmid for Horse GHRH.

US-11-186-282-33
 Query Match 33.6%; Score 1456.2; DB 12; Length 2700;
 Best Local Similarity 88.9%; Pred. No. 9.9e-198;

Matches 1663; Conservative 0; Mismatches 28; Indels 180; Gaps 1;
 QY 2462 AGAGCGGTTTGGCTATTGGAGCGCTTTCGCTTCTCTGCTCACTGACTGCTGCTGCTG 2521
 Db 859 AGTAGGGTTATTTGAGCTTGGCTTCCGCTTCTCTGCTCACTGACTGCTGCTGCTGCTG 918
 QY 2522 GTGCTGGCTGCGCGCGCGGCTGATACGCTCACTCAAAAGGGGTTAATCGGTTATCCCA 2581
 Db 919 GTGCTGGCTGCGCGCGGCTGATACGCTCACTCAAAAGGGGTTAATCGGTTATCCCA 978
 QY 2582 GAATCAGGGGTTAAACGACAGAAAGAACATGTGACCAAAAGGCCAGCAAAAGGCCAGAAC 2641
 Db 979 GAATCAGGGGTTAAACGACAGAAAGAACATGTGACCAAAAGGCCAGCAAAAGGCCAGAAC 1038
 QY 2642 GGTAAAAAGCGCGGTTGCTGCGCTTTCATAGGCTCGCGCCCTGACGAGCATAC 2701
 Db 1039 GGTAAAAAGCGCGGTTGCTGCGCTTTCATAGGCTCGCGCCCTGACGAGCATAC 1098
 QY 2702 AAAAATGACGCTCAAGTCAAGTGGGGAACCCGACAGGACTAATAAGATACAGGCG 2761
 Db 1099 AAAAATGACGCTCAAGTCAAGTGGGGAACCCGACAGGACTAATAAGATACAGGCG 1158
 QY 2762 TTTCCCGCTGGAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2821
 Db 1159 TTTCCCGCTGGAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218
 QY 2822 CTGTCGCGCTTTCCTCTTGGGAAAGCGTGGCGCTTTCATAGTCTCAAGCTGATGAT 2881
 Db 1219 CTGTCGCGCTTTCCTCTTGGGAAAGCGTGGCGCTTTCATAGTCTCAAGCTGATGAT 1278
 QY 2882 CTGAGTGGGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2941
 Db 1279 CTGAGTGGGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1338
 QY 2942 CCGGACGCTGCGCTTATCCGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3001
 Db 1339 CCGGACGCTGCGCTTATCCGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1398
 QY 3002 TTATGCGCATGCGACAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3061
 Db 1399 TTATGCGCATGCGACAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1458
 QY 3062 GCTACAGAGTCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3121
 Db 1459 GCTACAGAGTCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1518
 QY 3122 ATCTGCGCTGCTGAGCAGTACCTTCCGAAAAAGAGTTGGTAGCTCTTGAATCCGCGC 3181
 Db 1519 ATCTGCGCTGCTGAGCAGTACCTTCCGAAAAAGAGTTGGTAGCTCTTGAATCCGCGC 1578
 QY 3182 AAACAAACACCGCTGCTGAGCGGTTTCTTTTTCGACAGCAGAGATTACCGGCAGA 3241
 Db 1579 AAACAAACACCGCTGCTGAGCGGTTTCTTTTTCGACAGCAGAGATTACCGGCAGA 1638
 QY 3242 AAAAAGGATCTCAAGAAATCTTGAATCTTCTTCAAGGGGCTGACGCTCAGTGAAC 3301
 Db 1639 AAAAAGGATCTCAAGAAATCTTGAATCTTCTTCAAGGGGCTGACGCTCAGTGAAC 1692
 QY 3302 GAAAACTCAGCTTAAGGATTTTGGTATGACGCGATACATATTTGATGATTTAGAAA 3361
 Db 1693 ----- 1692
 QY 3362 AATAAACAATAGGGGTTCCGCGCACATTTCCGAAAAAGTCCACCTGTATGCGGTGTG 3421
 Db 1693 ----- 1692
 QY 3422 AATATCGCACAGATGCGTAAAGAAAATATCCGATCAGGAATGTGAACGTTAATAA 3481
 Db 1693 -----CTAGCG 1698
 QY 3482 TTCAAGAAACCTGCTCAAGAAAGGATGAAAGGCGATGCGCTGGAATCGGAGCGGCGA 3541
 Db 1699 CTCAGAGAACTGCTCAAGAAAGGATGAAAGGCGATGCGCTGGAATCGGAGCGGCGA 1758

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QY 3542 TACCGTAAAGCAGAGAAAGCGGTCAAGCCATTCGCCCGCAAGCTTTCAGCAATATAC 3601
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DB 1759 TACCGTAAAGCAGAGAAAGCGGTCAAGCCATTCGCCCGCAAGCTTTCAGCAATATAC 1818
QY 3602 GGGTAAAGCAGCTATGCTCTGATAGCGGTCCGACACCCAGCGGCGACAGTGCATGA 3661
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DB 1819 GGGTAAAGCAGCTATGCTCTGATAGCGGTCCGACACCCAGCGGCGACAGTGCATGA 1878
QY 3662 ATCCAGAAAGCGGCAATTTTCCACATGATATTCGGCAAGGAGCATCGCAGTGTCA 3721
    |||
DB 1879 ATCCAGAAAGCGGCAATTTTCCACATGATATTCGGCAAGGAGCATCGCAGTGTCA 1938
QY 3722 CGACAGATCTTCGCGGTCCGACAGTGTCTGAGCTTGGCAACATTCGGTGGCG 3781
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DB 1939 CGACAGATCTTCGCGGTCCGACAGTGTCTGAGCTTGGCAACATTCGGTGGCG 1998
QY 3782 CGAGCCCGTATGCTCTTGTGTCAGATCATCTGATCGACAAGACCGGCTTCATCCGAG 3841
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DB 1999 CGAGCCCGTATGCTCTTGTGTCAGATCATCTGATCGACAAGACCGGCTTCATCCGAG 2058
QY 3842 TACGCTGCTCGATGCGATGTTTCTGATGCTGATGCGAGGAGGATGACCGATCA 3901
    |||
DB 2059 TACGCTGCTCGATGCGATGTTTCTGATGCTGATGCGAGGAGGATGACCGATCA 2118
QY 3902 GCGTATGACGCGCGCGCATTCATCAGCCATGATGATATCTTCTTCGAGAGCAAGGT 3961
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DB 2119 GCGTATGACGCGCGCGCATTCATCAGCCATGATGATATCTTCTTCGAGAGCAAGGT 2178
QY 3962 GAGATGACAGAGATCTGCGCGCGCATTCGCGCGCATTCGAGAGGAGGATGACCGAT 4021
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DB 2179 GAGATGACAGAGATCTGCGCGCGCATTCGCGCGCATTCGAGAGGAGGATGACCGAT 2238
QY 4022 CAGTGAACAAGTGAAGCAGAGTGGCGAAGAAAGCGCGTCTGTCAGCCATGATGCG 4081
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DB 2239 CAGTGAACAAGTGAAGCAGAGTGGCGAAGAAAGCGCGTCTGTCAGCCATGATGCG 2298
QY 4082 GGGCTGCTCTGCTTTCAGTTCATTCAGGGCAACCGGAGAGTCCGCTTGAACAAAGAA 4141
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DB 2299 GGGCTGCTCTGCTTTCAGTTCATTCAGGGCAACCGGAGAGTCCGCTTGAACAAAGAA 2358
QY 4142 CCGGGGCGCGCTGCGCTGACAGCGCGAACAAGCGGCGCATCAGAGCAGCGATGCTGT 4201
    |||
DB 2359 CCGGGGCGCGCTGCGCTGACAGCGCGAACAAGCGGCGCATCAGAGCAGCGATGCTGT 2418
QY 4202 GTGCCAGTCATAGCCGAATAGCTCTCAACCCAGCGGCGGAGAACTGCGTCAATC 4261
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DB 2419 GTGCCAGTCATAGCCGAATAGCTCTCAACCCAGCGGCGGAGAACTGCGTCAATC 2478
QY 4262 CATCTGTCATCATGCGAAGAGATCTCATCTGCTCTTGATCAGAGCTTGATCCGC 4321
    |||
DB 2479 CATCTGTCATCATGCGAAGAGATCTCATCTGCTCTTGATCAGAGCTTGATCCGC 2538
QY 4322 TCGGCATCAG 4332
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DB 2539 TCGGCATCAG 2549
    |||

RESULT 14
US-10-764-818A-19
; Sequence 19, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASING CUI
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2716

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; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized ("GHRH") sequence for bovine.
US-10-764-818A-19
Query Match      33.6%; Score 1456.2; DB 7; Length 2716;
Best Local Similarity 88.9%; Pred. No. 9.9e-198;
Matches 1663; Conservative 0; Mismatches 28; Indels 180; Gaps 1;

QY 2462 AGAGCGGTTTTCGATTTGAGCGCTCTTCGCTTCTCTGCTCACTGACTCGTGGCTCG 2521
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DB 854 AGTGAAGGTAAATTTCAGCTTGTGCTTCCGCTTCTGCTCACTGACTCGTGGCTCG 913
QY 2522 GTTCGTCGCTTCGCGCGCGGATTCAGCTTCACTCACTCAAGGCGGTAAATCGGTTATCCACA 2581
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DB 914 GTTCGTCGCTTCGCGCGCGGATTCAGCTTCACTCACTCAAGGCGGTAAATCGGTTATCCACA 973
QY 2582 GAATCAGGAGATTAACGAGAAAGAAACATGTAGCAAAAGGCGACGAAAGGCGAGAAC 2641
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DB 974 GAATCAGGAGATTAACGAGAAAGAAACATGTAGCAAAAGGCGAGAAAGGCGAGAAC 1033
QY 2642 CGTAAAGAGCGCGCTTCTGCTGCTTTCATAGGCTCCGCGCTGACGAGCATAC 2701
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QY 2702 AAAAATCGACCTCAAGTCAAGAGGTGGGAAACCGGACAGATTAAGATACAGGCG 2761
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DB 1094 AAAAATCGACCTCAAGTCAAGAGGTGGGAAACCGGACAGATTAAGATACAGGCG 1153
QY 2762 TTTCCCGTGAAGCTCCCTGCTGCTCTCTGTTCCGACCTTCGCGCTTACCGGATAC 2821
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DB 1154 TTTCCCGTGAAGCTCCCTGCTGCTCTCTGTTCCGACCTTCGCGCTTACCGGATAC 1213
QY 2822 CTGTCGCTTCTTCCTTCGGAAGAGTGGCGCTTCTCAATGCTCAAGCTGTAGAT 2881
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DB 1214 CTGTCGCTTCTTCCTTCGGAAGAGTGGCGCTTCTCAATGCTCAAGCTGTAGAT 1273
QY 2882 CTCACTTGGGTAGTGGTGGTTCGTCGAAGCTGGGCTGTTGTCAGAACCCCGCTTCAG 2941
    |||
DB 1274 CTCACTTGGGTAGTGGTGGTTCGTCGAAGCTGGGCTGTTGTCAGAACCCCGCTTCAG 1333
QY 2942 CCCGACCGCTGCGCTTATCCGTTAACTACTCTTTGAGTCCAACCCGTTAAGACAGAC 3001
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DB 1334 CCCGACCGCTGCGCTTATCCGTTAACTACTCTTTGAGTCCAACCCGTTAAGACAGAC 1393
QY 3002 TTATGCGCATGCGCAGACGCACTGTGTAACAGATTTAGCAGAGCGATATGAGCGGT 3061
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DB 1394 TTATGCGCATGCGCAGACGCACTGTGTAACAGATTTAGCAGAGCGATATGAGCGGT 1453
QY 3062 GCTACAGAGTTCTTAAGTGTGGGCTTAACCTACGCGTACACTAGAAAGCAGATTTGGT 3121
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DB 1454 GCTACAGAGTTCTTAAGTGTGGGCTTAACCTACGCGTACACTAGAAAGCAGATTTGGT 1513
QY 3122 ATCTGCGCTCTGCTGAAGCAGCTTACCTTCGAAAAAGATTGTAAGCTTTCGCGC 3181
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DB 1514 ATCTGCGCTCTGCTGAAGCAGCTTACCTTCGAAAAAGATTGTAAGCTTTCGCGC 1573
QY 3182 AAACAAACACCGCTGTGTAGCGGTGTTTTTTTGTTCGACAGAGATTAAGCGGCA 3241
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DB 1574 AAACAAACACCGCTGTGTAGCGGTGTTTTTTTGTTCGACAGAGATTAAGCGGCA 1633
QY 3242 AAAAAGAGATCAAGAAAGATCTTTCATCAGGAGGTGACGCTCAGTGGAGAC 3301
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DB 1634 AAAAAGAGATCAAGAAAGATCTTTCATCAGGAGGTGACGCTCAGTGGAGAC 1687
QY 3302 GAAATCACTTAAGGAGTTTGTGTCATGAGCGGATACATATTGAATGATTAGAAA 3361
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DB 1688 ----- 1687
QY 3362 AATTAACAAATAGGGGTTCCGCGACATTTCCCGGAAAGTGCCACCTGTATGGGTGTG 3421
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Search completed: March 15, 2006, 23:47:20
Job time : 1215 secs

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Db 1688 ----- 1687
QY 3422 AAATACCCACAGATGCGTAAGAGAAAAATACCGCATCAGAAATTGTAGCGTTAATPA 3481
Db 1688 -----CTAGCG 1693
QY 3482 TTCAGAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCCAATCGGAGCGGCGA 3541
Db 1694 CTCAGAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCCAATCGGAGCGGCGA 1753
QY 3542 TACCGTAAAGCAGAGAAAGCGGTGAGCCCATTTGCGCGCAAGCTCTTCAGCAATATCAC 3601
Db 1754 TACCGTAAAGCAGAGAAAGCGGTGAGCCCATTTGCGCGCAAGCTCTTCAGCAATATCAC 1813
QY 3602 GGGTAGCCAAAGCTATGTCCTGATAGCGGTCCGCCAACCCAGCCGCGCACAGTCATGA 3661
Db 1814 GGGTAGCCAAAGCTATGTCCTGATAGCGGTCCGCCAACCCAGCCGCGCACAGTCATGA 1873
QY 3662 ATCCAGAAAAGCGCCATTTTCCACCATGATATTTGGGCAAGCAGCATGCGCATGGTCA 3721
Db 1874 ATCCAGAAAAGCGCCATTTTCCACCATGATATTTGGGCAAGCAGCATGCGCATGGTCA 1933
QY 3722 CGACGAGATCCTCGCGGTGGGCGATGCTGGCCTTGAGCCTGGCGAAAGTTGCGTGGCG 3781
Db 1934 CGACGAGATCCTCGCGGTGGGCGATGCTGGCCTTGAGCCTGGCGAAAGTTGCGTGGCG 1993
QY 3782 CGAGCCCTGATGCTCTTGTGTCAGATCATCTGATCGAACAAAGCCGCTTCCATCCGAG 3841
Db 1994 CGAGCCCTGATGCTCTTGTGTCAGATCATCTGATCGAACAAAGCCGCTTCCATCCGAG 2053
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Db 2054 TACGTGCTCGTGGATGCGATGTTTGCTTGGTGGTGCATGGGCGAGTACCGGATCAA 2113
QY 3902 GGGTATGCAAGCCGCGCATTTGATCAGCATGATGATATCTTCTCGCAGAGCAAGGT 3961
Db 2114 GGGTATGCAAGCCGCGCATTTGATCAGCATGATGATATCTTCTCGCAGAGCAAGGT 2173
QY 3962 GAGATGACAGAGATCTGCCCCGAGCATTTGCCCAATAGCAAGCCAGTCTTCCGCTT 4021
Db 2174 GAGATGACAGAGATCTGCCCCGAGCATTTGCCCAATAGCAAGCCAGTCTTCCGCTT 2233
QY 4022 CAGTGCAACGTGAGACACAGCTGCCCAAGAACCCCGCTCGTGGCCAGCAAGATAGCC 4081
Db 2234 CAGTGCAACGTGAGACACAGCTGCCCAAGAACCCCGCTCGTGGCCAGCAAGATAGCC 2293
QY 4082 GCGCTGCTCGTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 4141
Db 2294 GCGCTGCTCGTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2353
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Db 2354 CCGGGGGCCCTGCGCTGACAGCGGAAACAGCGGCGATCAGACAGCCGATTTGCTGTT 2413
QY 4202 GTGCCCAATATAGCCGAATAGCTTCCCAACCCAGCGCGGAGAACCTGCGTGCATC 4261
Db 2414 GTGCCCAATATAGCCGAATAGCTTCCCAACCCAGCGCGGAGAACCTGCGTGCATC 2473
QY 4262 CATCTTGTCAATCATGCGAAAGCATCTCATCTTGTATCAGAGCTTATCCC 4321
Db 2474 CATCTTGTCAATCATGCGAAAGCATCTCATCTTGTATCAGAGCTTATCCC 2533
QY 4322 TCGCCATCAG 4332
Db 2534 TCGCCATCAG 2544
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